

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 02:52:41 ; Search time 9525 Seconds  
(without alignments)  
11079.838 Million cell updates/sec

Title: US-10-617-623-1

Perfect score: 2178

Sequence: 1 cctctctgttcttctctctg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1617	74.2	1617	6	CQ805714 Sequence
2	1617	74.2	1617	6	AX506544 Sequence
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4	1614	74.1	1614	8	AF106324 Arabidops
5	1610.6	73.9	1617	8	AF685183 Arabidops
6	1610.6	73.9	1617	8	AF510074 Arabidops
7	1180	54.2	1723	8	AF189676 Brassica
8	1141.8	52.4	1641	8	AF490586 Arabidops
9	889.6	40.8	2135	8	AY028416 Citrus x
10	889.4	40.8	2485	8	AF515632 Gossypium
11	858	39.4	1752	8	AY513732 Medicago
12	858	39.4	2232	8	AY456096 Medicago
13	833.4	38.3	1656	8	AY371319 Chenopodi
14	832.8	38.2	1668	6	E63046 Na+/H+ anti
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18	821.6	37.7	1668	8	AY211397 Atriplex
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21	813	37.3	2423	6	BD012814	BD012814 Gene codi
22	813	37.3	2423	6	AB051817	AB051817 Petunia x
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25	786	36.1	2109	8	AY730277	AY730277 Iris lact
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32	768	35.3	2133	8	AY261806	AY261806 Suaeda ma
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#### ALIGNMENTS

RESULT 1  
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LOCUS CQ805714 1617 bp DNA linear PAT 10-MAY-2004  
DEFINITION Sequence 2125 from Patent WO2004035798.  
ACCESSION CQ805714  
VERSION CQ805714.1 GI:47111491  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
AUTHORS Inze,D., de Veylder,L. and Vlieghe,K.  
TITLE Identification of novel e2f target genes and use thereof  
JOURNAL Patent: WO 2004035798-A 2135 29-APR-2004;  
Croppesign N.V. (BE)  
FEATURES  
source Location/Qualifiers  
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#### ORIGIN

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Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 346 GTTGGCTTGAATCTCTTTTGTGCTTCTTTTGTGCTTGTATTGTTCTTGTCTATCTTTTG 405  
DB 61 GTTGGCTTGAATCTCTTTTGTGCTTCTTTTGTGCTTGTATTGTTCTTGTCTATCTTTTG 120  
QY 406 GAAGAGATAGATGATGAACCAATCCATCACCCTTCTTGTGATGGCTAGGCTAGTGT 465  
DB 121 GAAGAGATAGATGATGAACCAATCCATCACCCTTCTTGTGATGGCTAGGCTAGTGT 180  
QY 466 GTTACCATTTCTTGTATTAGTAAGAAAGCTGCTATCTTCTCTCTTTTAGTGAAGAT 525

181	Db	GT	TACCACTTTTGTGATAGTAAAGGAAAAAGCTCGCAGTCTTCTCGTCTTTAGTGAAGAT	240
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586	Qy	AAG	CAGTTTTTCGCAATTTTGGTACACTATATGCTTTTGGTGTCTGTTGGGACTATATAT	645
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646	Qy	TC	TGTGCACAAATCATATCTAGGTGTAAACACAGTTCCTTTAAGAAAGTTGGACATTTGGAAAC	705
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706	Qy	TT	TGACTTGGGTGATATCTTCTATTTGGTGCCTATATTTGGTGCCTGCAACAGATTCAGTATGT	765
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481	Db	AC	CTGCAGGTTCTGAATCAAGACGACACCTTTTGTCTTTACAGTCTTTGTATTCGGAGAG	540
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Db	1561	CCCTTTGTTCCAGGTCTCCAACTGAGAGAAACCTCCCTGATCTTATAGTAAGGCTTGA	1617
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AX506544.1 GI:23387781			
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Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsais.			
1			
Harper, J.F., Kleps, J., Wang, X. and Zhu, T.			
Stress-regulated genes of plants, transgenic plants containing same, and methods of use			
Patent: WO 0216655-A 1239 28-FEB-2002;			
The Scripps Research Institute (US) ; Syngenta Participations AG			
(CH)			
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Query Match			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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LOCUS AF056190 1619 bp mRNA linear PLN 06-JUN-2000
DEFINITION Arabidopsis thaliana Na+/H+ exchanger (NHX1) mRNA, complete cds.
ACCESSION AF056190
VERSION AF056190.1 GI:6650176
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1619)
AUTHORS Quintero, F.J., Blatt, M.R. and Pardo, J.M.
TITLE Functional conservation between yeast and plant endosomal
Na(+)/H(+) antiporters
JOURNAL FEBS Lett. 471 (2-3), 224-228 (2000)
MEDLINE 20231718
PUBMED 10767428
REFERENCE 2 (bases 1 to 1619)
AUTHORS Quintero, F.J.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1998) Biologia Vegetal, IRNASE (CSIC), Avda.
Reina Mercedes s/n, Sevilla 41012, Spain
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ORIGIN
Query Match 74.2%; Score 1615.8; DB 8; Length 1619;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4  
AF106324

LOCUS AF106324 1614 bp mRNA linear PLN 03-MAR-1999  
DEFINITION Arabidopsis thaliana sodium proton exchanger Nhx1 mRNA, partial  
cDS.  
ACCESSION AF106324  
VERSION AF106324.1 GI:4324596  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1614)  
AUTHORS Gaxiola, R.A., Rao, R., Sherman, A., Grisafi, P., Alper, S.L. and Fink, G.R.

TITLE The Arabidopsis thaliana proton transporters, AtNhx1 and Avp1, can function in cation detoxification in yeast  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1480-1485 (1999)  
MEDLINE 99145575  
PUBMED 9990049

REFERENCE 2 (bases 1 to 1614)  
AUTHORS Gaxiola, R.A., Rao, R., Sherman, A., Grisafi, P., Alper, S.L. and Fink, G.R.

TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1998) Whitehead, Nine Cambridge Center, Cambridge, MA 02142, USA

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Location/Qualifiers  
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## ORIGIN

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## RESULT 5

AY685183

LOCUS

DEFINITION

Arabidopsis thaliana

cds.

ACCESSION

AY685183

VERSION

AY685183.1

KEYWORDS

ORGANISM

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.

1 (bases 1 to 1617)

Wang, D., Zhang, J.L. and Zhang, J.W.

Direct Submission

Submitted (14-JUL-2004) Agronomy College, Institute of

Agrobiotechnology, Lanzhou, Gansu 730070, China

Location/Qualifiers

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/organism="Arabidopsis thaliana"

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1. .1617

gene



AUTHORS Baek,S.H.  
TITLE Isolation and characterization of a Na<sup>+</sup>/H<sup>+</sup> antiporter gene from Arabidopsis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1617)  
AUTHORS Baek,S.H., Kim,H.S., Lee,Y.T., Lee,M.H. and Yun,S.J.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAY-2002) Rice Research Division, National Honam Agricultural Experiment Station, Songhak-dong, Iksan, Jeonbuk 570-080, Republic of Korea

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RESULT 8
AF490586      1641 bp mRNA linear PLN 04-APR-2002
LOCUS      Arabidopsis thaliana Na+/H+ exchanger 2 (NHX2) mRNA, complete cds.
DEFINITION
ACCESSION      AF490586
VERSION
SOURCE
KEYWORDS
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1641)
Yokoi,S., Quintero,F.J., Cubero,B., Ruiz,T., Bressan,R.A.,
Hasegawa,P.M. and Pardo,J.M.
Differential expression and function of Arabidopsis thaliana NHX
Na+/H+ antiporters in the salt stress response
Plant J. (2002) In press
2 (bases 1 to 1641)
Quintero,F.J., Cubero,B. and Pardo,J.M.
Direct Submission
Submitted (07-WAR-2002) Biologia Vegetal, IRNASA-CSIC, Avda. Reina
Mercedes, 10, Sevilla, Sevilla 41012, Spain
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## ORIGIN

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DEFINITION  
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AY513732  
VERSION  
AY513732.1 GI:46250920  
KEYWORDS  
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SOURCE  
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REFERENCE  
1 (bases 1 to 1752)  
An, B.Y. and Zhang, X.S.  
Isolation and expression of MsNHX1 gene in alfalfa  
Unpublished  
JOURNAL  
REFERENCE  
2 (bases 1 to 1752)  
An, B.Y. and Zhang, X.S.  
Direct Submission  
JOURNAL  
Submitted (27-DEC-2003) College of Life Sciences, Shandong  
Agricultural University, Daizong Street, Taian, Shandong 271018,  
P.R. China  
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DEFINITION Medicago sativa Na+/H+ antiporter mRNA, complete cds.
ACCESSION AY456096
VERSION AY456096.1 GI:38373524
KEYWORDS Medicago sativa
SOURCE Medicago sativa
ORGANISM Medicago sativa
REFERENCE 1 (bases 1 to 2232)
AUTHORS Yang,Q.C., Wu,M.S. and Wang,P.Q.
TITLE The gene encoding Na+/H+ antiporter cloned from alfalfa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2232)
AUTHORS Yang,Q.C., Wu,M.S. and Wang,P.Q.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2003) Turf & Forage Science, Chinese Academy of
Agricultural Science (CAAS), No.2 Yuanmingyuan West Road, Haidin,
Beijing 100094, China
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DEFINITION	Chenopodium glaucum Na+/H+ antiporter (NHX) mRNA, complete cds.	
ACCESSION	AV371319	
VERSION	AV371319.1	GI:34484303
KEYWORDS		microchondrion Chenopodium glaucum
SOURCE		Chenopodium glaucum
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Chenopodium.
REFERENCE		1 (bases 1 to 1656)
AUTHORS		Li, J., Zhang, F., Ma, J., Cai, L. and Wang, Y.
TITLE		Using RT-PCR to Amplify the NHX Gene Fragment in Chenopodium glaucum
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 1656)
AUTHORS		Zhang, F., Li, J., Ma, J., Cai, L. and Wang, Y.
TITLE		Direct Submission
JOURNAL		Submitted (20-AUG-2003) College of Life Science and Technology, Xinjiang University, 14 Shengli Road, Urumqi, Xinjiang 830046, China
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PC	C12N15/09, A01H5/00, C07K14/415, C12Q1/68//C12N5/10, C12N15/00, PC C12N5/00	
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QY	383 GTATGTTCTTGGTTCATCTTTTGAAGAGAAATAGATGATGAAGCAATCCATCAACGCGCT	442
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QY	443 TGTGATTTGGCTAGGCACTGGTGTACCAATTTGTTGATTTAGTAGTAAGAGAAAGCTTCGC	502
DB	170 TTCTTATAGGTTTGGCTACTGGGTTCTGTGATCTGCTGATTTAGTAGGAGGAGAAAGTTAC	229
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DB	530 TCTACAGTCTGGTCTTTGGGAGGAGGTTGTTGTAATGATGCAATCAGTGGTCTTTTCA	589
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DEFINITION	Na+/H+ antiporter protein and gene encoding it.	PAT 31-JAN-2002
ACCESSION	E63047	
VERSION	E63047.1	GI:18628472
KEYWORDS	JP 2000157287-A/2.	
SOURCE	unidentified	
ORGANISM	unclassified	
REFERENCE	1 (bases 1 to 1668)	
AUTHORS	Shono, M., Hayakawa, T. and Tanaka, A.	
TITLE	Na+/H+ antiporter protein and gene encoding it	
JOURNAL	Patent: JP 2000157287-A 2 13-JUN-2000;	
	PLANTECH RESEARCH INSTITUTE	



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	PD	13-JUN-2000	
	PF	16-SEP-1999	JP 1999261606
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QY	323	CGACATCTGATCAGCTTCTGTGGTTCGCTTGAATCTCTTTGTGCACTTCTTTGTGCTT	382
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## RESULT 2

US-10-617-624-1

; Sequence 1, Application US/10617624

; Publication No. US20050034191A1

; GENERAL INFORMATION:

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; APPLICANT: Blumwald, Eduardo
; TITLE OF INVENTION: SALT TOLERANT OIL CROPS
; FILE REFERENCE: 529642000500
; CURRENT APPLICATION NUMBER: US/10/617,624
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 60/395,656
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 38
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; SEQ ID NO 1
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DB 181 AGACTTTTTTTTCCAGATTTGCTGATCCAAAATCTGAATAGTTGTTTCAATGTTCTTGAT 240
QY 241 CAAATCTGAAGAAGAAGTTGTTGCGATCTAGAAGAAGATAACAATGTTGATCTCTA 300
DB 241 CAAATCTGAAGAAGAAGTTGTTGCGATCTAGAAGAAGATAACAATGTTGATCTCTA 300
QY 301 GTGTCGAAATCGCTTCTGTTATCGACATCTGATCAGCTTCTGTTGTTGTTGAATCTC 360
DB 301 GTGTCGAAATCGCTTCTGTTATCGACATCTGATCAGCTTCTGTTGTTGTTGAATCTC 360
QY 361 TTTGTTGCACTTCTTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 420
DB 361 TTTGTTGCACTTCTTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 420
QY 421 ATGAACGAATCCATACCCGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
DB 421 ATGAACGAATCCATACCCGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
QY 481 ATTAGTAAAGGAAAGCTCGCATCTCTGCTTTTGTAGTGAAGATCTTTTCTCATATAT 540
DB 481 ATTAGTAAAGGAAAGCTCGCATCTCTGCTTTTGTAGTGAAGATCTTTTCTCATATAT 540
QY 541 CTTTGTGCCACCCATATATTTCAATGAGGGTTTCAAGTAAAGAAAGAGAGAGTTTTCGCG 600
DB 541 CTTTGTGCCACCCATATATTTCAATGAGGGTTTCAAGTAAAGAAAGAGAGAGTTTTCGCG 600
QY 601 AATTTCGTGACTATTAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
DB 601 AATTTCGTGACTATTAATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 660
QY 661 TCTCTAGGTGTAACACAGTCTTTTAAAGAGTTGGAATTTGGAACCTTTGAGTGGGTGAT 720
DB 661 TCTCTAGGTGTAACACAGTCTTTTAAAGAGTTGGAATTTGGAACCTTTGAGTGGGTGAT 720
QY 721 TATCTTGTCTATTGTTGCCATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
DB 721 TATCTTGTCTATTGTTGCCATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
QY 781 AATCAAGACGAGACACCTTGTCTTATAGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 840
DB 781 AATCAAGACGAGACACCTTGTCTTATAGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 840
QY 841 GCAACGTCTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 900
DB 841 GCAACGTCTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 900
QY 901 GAAGCTGCTTTTCACTTCTTGGAAACCTTCTTGTATTTGTTGTTGTTGTTGTTGTTGTTG 960
DB 901 GAAGCTGCTTTTCACTTCTTGGAAACCTTCTTGTATTTGTTGTTGTTGTTGTTGTTGTTG 960
QY 961 GGTGCTGCAACCGGCTCTGATAAGTGTGTTTATCAAGAGCTATACCTTTGGAAGGCAC 1020
DB 961 GGTGCTGCAACCGGCTCTGATAAGTGTGTTTATCAAGAGCTATACCTTTGGAAGGCAC 1020
QY 1021 TCAACTGACCGAGAGGTTGCTTATGATGCTTATGCGCTATCTTTCTTATATGCTTGCT 1080
DB 1021 TCAACTGACCGAGAGGTTGCTTATGATGCTTATGCGCTATCTTTCTTATATGCTTGCT 1080
QY 1081 GAGCTTTTTCGACTTGAAGCGGTTATCTCTACTGTTGTTTCTGTTGTTGTTGTTGTTGTTG 1140
DB 1081 GAGCTTTTTCGACTTGAAGCGGTTATCTCTACTGTTGTTTCTGTTGTTGTTGTTGTTGTTG 1140
QY 1141 TACACATGSCACAATGTTACGAGAGCTCAAGAAATAACAACAAGCATACCTTTTGAAC 1200
DB 1141 TACACATGSCACAATGTTACGAGAGCTCAAGAAATAACAACAAGCATACCTTTTGAAC 1200
QY 1201 TTGTCATTTCTTTCGCGAGACATTTATTTTCTTGTATGTTGGAATGATGCTTTGACAT 1260
DB 1201 TTGTCATTTCTTTCGCGAGACATTTATTTTCTTGTATGTTGGAATGATGCTTTGACAT 1260
QY 1261 GACAAAGTGAGATTCGTTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTTA 1320
DB 1261 GACAAAGTGAGATTCGTTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTTA 1320
QY 1321 ATGGGCTCTGCTCATGTTGGAAGAGCAGGTTGCTGTTTCCGTTATCGTTTCTATCTAAC 1380
DB 1321 ATGGGCTCTGCTCATGTTGGAAGAGCAGGTTGCTGTTTCCGTTATCGTTTCTATCTAAC 1380
QY 1381 TTAGCCAAAGAAGAAATCAAAAGCAGAGAAATCAAACTTTTAAATGAGGTTGTTGTTGTTG 1440
DB 1381 TTAGCCAAAGAAGAAATCAAAAGCAGAGAAATCAAACTTTTAAATGAGGTTGTTGTTGTTG 1440
QY 1441 TCTGTTCTCATGAGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
DB 1441 TCTGTTCTCATGAGAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
QY 1501 GGGCACACAGATGTACGCGGGAATGCAATCATGATCAGGATCAGATACGATGTTGTTGTTG 1560
DB 1501 GGGCACACAGATGTACGCGGGAATGCAATCATGATCAGGATCAGATACGATGTTGTTGTTG 1560
QY 1561 TTTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1620
DB 1561 TTTAGCACAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1620
QY 1621 CAGAACGCCACCAACGAGATGTTATCTGATGACACACCCCAAAATCCATATATCCCT 1680
DB 1621 CAGAACGCCACCAACGAGATGTTATCTGATGACACACCCCAAAATCCATATATCCCT 1680
QY 1681 TTTGTTGGACCAAGACTCGTTTCAATGAGCTTCAAGGAAACCAATGTTGCTCGGCTGAC 1740
DB 1681 TTTGTTGGACCAAGACTCGTTTCAATGAGCTTCAAGGAAACCAATGTTGCTCGGCTGAC 1740
QY 1741 AGTATACGTGGCTTCTTGGACGCGGCTCAAGACCGTCAATTTATCTGAGAGCAATTT 1800
DB 1741 AGTATACGTGGCTTCTTGGACGCGGCTCAAGACCGTCAATTTATCTGAGAGCAATTT 1800
QY 1801 GATGACTCTTTCATGCGACCCCTCTTTGAGGCTGTTGAGGCTGTTGATCCCTTTGTTCCAGGT 1860
DB 1801 GATGACTCTTTCATGCGACCCCTCTTTGAGGCTGTTGAGGCTGTTGATCCCTTTGTTCCAGGT 1860
QY 1861 TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTATAGGCTTGAAGGTTAAAGTGAAGAAA 1920
DB 1861 TCTCCAACTGAGAGAAACCTCTCTGATCTTAGTATAGGCTTGAAGGTTAAAGTGAAGAAA 1920
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Db 1381 TCCATACATATCCCTTTGTTGACCAAGACTCGTTCAATGAGCCTTCAGGGAACCAAT 1440
Qy 1726 GTGCTCGGCTGACAGTATACGTGGCTCTTGACACGGCCCACTCGAAACCGTGCAATTAC 1785
Db 1441 GTGCTCGGCTGACAGTATACGTGGCTCTTGACACGGCCCACTCGAACCGTGCAATTAC 1500
Qy 1786 TACTGAGACAAATTTGATGACTCTTTCATCGGACCGCTCTTTGGAGTCTGGCTTTGTA 1845
Db 1501 TACTGAGACAAATTTGATGACTCTTTCATCGGACCGCTCTTTGGAGTCTGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCCAGGTCTCCAACTGAGAGAAACCTCCCTGATCTTAGTAGAGGCTTGA 1902
Db 1561 CCCTTTGTTCCAGGTCTCCAACTGAGAGAAACCTCCCTGATCTTAGTAGAGGCTTGA 1617

RESULT 4
US-09-938-842A-1239
; Sequence 1239, Application US/09938842A
; Publication No. US2004009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepb, Joel
; APPLICANT: Wang, Jun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1239
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1239

Query Match 74.2%; Score 1617; DB 11; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 286 ATGTTGGATTCTCTAGTGTGGAACCTGCTTGGTTATCGACATCTGATCAGCTTCTGTG 345
Db 1 ATGTTGGATTCTCTAGTGTGGAACCTGCTTGGTTATCGACATCTGATCAGCTTCTGTG 60
Qy 346 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGCTTGTATGTTCTTGTGTCATCTTTTG 405
Db 61 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGCTTGTATGTTCTTGTGTCATCTTTTG 120
Qy 406 GAAGAGAATAGATGATGAACGAATCCATCACCCTGTTGTTGATGGGCTAGGCACTGGT 465
Db 121 GAAGAGAATAGATGATGAACGAATCCATCACCCTGTTGTTGATGGGCTAGGCACTGGT 180
Qy 466 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTGCTTTTAGTGAAGAT 525
Db 181 GTTACCAATTTGTTGATTAGTAAGGAAAAGCTCGCATCTTCTGCTTTTAGTGAAGAT 240
Qy 526 CTTTCTTCATATATCTTTTGGCAACCCATATATTCATGACGGTTTCAAGTAAAAAAG 585
Db 241 CTTTCTTCATATATCTTTTGGCAACCCATATATTCATGACGGTTTCAAGTAAAAAAG 300
Qy 586 AAGCAGTTTTTCCGCAATTTCTGACTATTTATGCTTTTGGTGTGTTGGGACTATTATT 645
Db 301 AAGCAGTTTTTCCGCAATTTCTGACTATTTATGCTTTTGGTGTGTTGGGACTATTATT 360
Qy 646 TCTTGCACAATCATATCTCTAGGTGTAAACAGTTCTTTTAAAGATTGGACATTTGNAACC 705
Db 1
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Db 361 TCTTGCACAATCATATCTCTAGGTGTAAACAGTTCTTTTAAAGATTGGACATTTGNAACC 420
Qy 706 TTTGACTTGGGTGATTAATCTTGTATTTGGTCCCATATTTGCTGCAACAGATTCAGTATGT 765
Db 421 TTTGACTTGGGTGATTAATCTTGTATTTGGTCCCATATTTGCTGCAACAGATTCAGTATGT 480
Qy 766 AACTGCGAGTTCTGATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTTGCGAGAG 825
Db 481 ACATGTCAGGTTCTGATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTTGCGAGAG 540
Qy 826 GGTGTTGTGAATGATGCAACAGTTCAGTTGTGTTCTTCAAGCGGATTTCAGAGCTTTGTATCTC 885
Db 541 GGTGTTGTGAATGATGCAACAGTTCAGTTGTGTTCTTCAAGCGGATTTCAGAGCTTTGTATCTC 600
Qy 886 ACTCACCTAAACCAACGAGCTGCTTTTCATCTTTTGGAAACTTCTTGTATTTGTTTCTC 945
Db 601 ACTCACCTAAACCAACGAGCTGCTTTTCATCTTTTGGAAACTTCTTGTATTTGTTTCTC 660
Qy 946 CTAAGTACCTTGTGTTGCTGCAACCGCTCTGATAAGTGGCTATCTTATCAAGAGACTA 1005
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGCTCTGATAAGTGGCTATCTTATCAAGAGACTA 720
Qy 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 1065
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTT 780
Qy 1066 TCTTATATCTTGTCTGAGCTTTTCGACTTGGAGCGTATCTCTACTGTGTTTCTGTGGT 1125
Db 781 TCTTATATCTTGTCTGAGCTTTTCGACTTGGAGCGTATCTCTACTGTGTTTCTGTGGT 840
Qy 1126 ATTGTGATGTCCTCATTTACATGCGGCAATGTAACGAGAGCTCAAGATTAACAACAAAG 1185
Db 841 ATTGTGATGTCCTCATTTACATGCGGCAATGTAACGAGAGCTCAAGATTAACAACAAAG 900
Qy 1186 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245
Db 901 CATACCTTTGCAACTTTTGTCTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960
Qy 1246 GATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATGCA 1305
Db 961 GATGCTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATGCA 1020
Qy 1306 GTGAGCTCAATCTTAATGGGTCTGTCATGTTGGAAGAGCAGCTTCTGTTTCCGTTA 1365
Db 1021 GTGAGCTCAATCTTAATGGGTCTGTCATGTTGGAAGAGCAGCTTCTGTTTCCGTTA 1080
Qy 1366 TCGTTTCTATCTAACTTTAGCAGAGAAATCAAGCGAGAAATCAACTTTTAAACATGCGAG 1425
Db 1081 TCGTTTCTATCTAACTTTAGCAGAGAAATCAAGCGAGAAATCAACTTTTAAACATGCGAG 1140
Qy 1426 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATGCTCTTGTGATACAAC 1485
Db 1141 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATGCTCTTGTGATACAAC 1200
Qy 1486 AGTTTACAAAGGCGCGGCAACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1545
Db 1201 AGTTTACAAAGGCGCGGCAACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1260
Qy 1546 ATAACCTGCTGCTTTTGTAGCAGTGTGTTTGTGATGCTGACCAAAACCACTCATTAAGC 1605
Db 1261 ATAACCTGCTGCTTTTGTAGCAGTGTGTTTGTGATGCTGACCAAAACCACTCATTAAGC 1320
Qy 1606 TACTTATTACCGCACAGAACCGCACACGAGCATGTTATCTGATGACAAACACCCCAAAA 1665
Db 1321 TACTTATTACCGCACAGAACCGCACACGAGCATGTTATCTGATGACAAACACCCCAAAA 1380
Qy 1666 TCCATACATATCTCTTTGTTGGACCAAGACTCGTTCAATTGAGCCTTCAGGGAACCAAT 1725
Db 1381 TCCATACATATCTCTTTGTTGGACCAAGACTCGTTCAATTGAGCCTTCAGGGAACCAAT 1440
Qy 1726 GTGCTTGGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGTGCAATTAC 1785
Db 1441 GTGCTTGGGCTGACAGTATAGTGGCTTCTTGACACGGCCCACTCGAACCGTGCAATTAC 1500
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Qy 1786 TACTGGAGACAATTGTAGTACTCTCATGCGACCCGCTTTTGAGAGTCGTCGGCTTTGTA 1845
Db 1501 TACTGGAGACAATTGTAGTACTCTCATGCGACCCGCTTTTGAGAGTCGTCGGCTTTGTA 1560
Qy 1846 CCCTTTGTTCAGGTTCTCCAACTGAGAGAAACCCCTCCTCATCTTACTAGGCTTGA 1902
Db 1561 CCCTTTGTTCAGGTTCTCCAACTGAGAGAAACCCCTCCTCATCTTACTAGGCTTGA 1617

RESULT 5
US-10-155-535-1
; Sequence 1, Application US/10155535
; Publication No. US20030046729A1
; GENERAL INFORMATION:
; APPLICANT: Blumwald, Eduardo
; APPLICANT: Apepe, Maris
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTIPOETERS
; FILE REFERENCE: 529152000720
; CURRENT APPLICATION NUMBER: US/10/155,535
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/271,584
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,474
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: 60/116,111
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-155-535-1

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Db	833	 CCGACTCTGTATGACACCTACAGGTTCTCAATCAAGATGAGACACCTTTGCTTTACAGTC	892
Qy	812	TTGTATTCCGAGAGGGTGTGTGAATGATGCAACGTCAGTTGTGGTCTTCAACGCGGATTC	871
Db	893	TTGTATTGGAGAGGGGTGTGAATGATGCCACATCTGTGTGTCTTTCATATGCTATTTC	952
Qy	872	AGAGCTTTGATCTCAGTCACCTAAACCAACGAAAGTGTCTTTTCATCTTCTTTGGAACCTTCT	931
Db	953	AGAGTTTGGACCTCACCACCTTAACCATGAAGCAGCTTTTTCATTTCTTTGGGAACTTTT	1012
Qy	932	TGTAATTTGTTTCTCCTAAAGTACCTTGTCTGGTCTGCAACCGGCTGTATGAAGTGCCTATG	991
Db	1013	TTTATCTGTTTCTCTTGAGCACCGGACTTGGTGTGCGCACTGTGTCTGTATGAAGTGCCTATG	1072
Qy	992	TTATCAAGAAGCTATACCTTTTGGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTTATGATGC	1051
Db	1073	TCATCAAGAAACGTATTTTGGGAAGGCACCTCGACTGATCGAGAAGTTGGCCCTCATGATGC	1132
Qy	1052	TTATGGGCTATCTTCTTATATGCTGTCTGAGCTTTTTCGACTTTGAGGGGTATCTCTCACTG	1111
Db	1133	TTATGGGCTTATCTTTCATATGCTTGTCTGAGCTATTCGCTTTGAGTGTGATCCTTAACCTG	1192
Qy	1112	TGTTTTTCTGTGGTATTGTGATGTCCCATTAACATGCGACAAATGTAAACGGAGAGCTCAA	1171
Db	1193	TATTTTCTGTGGGATTGTGATGTGCCATTAACCTTGGCACATGTCAACGAGAGCTCAA	1252
Qy	1172	GAATAAACAACAAGCATACCTTTTGCAACTTTTGTCTATTTCTTGGGAGACAATTTATTTTCT	1231
Db	1253	GAATTAACCAAGCATGCGCTTTTGCTACTTTGTCTGTCTCGCTGAGACTTTTATTTTCTC	1312
Qy	1232	TGTATGTTGGAAATGGAATCTGACATTCGACAAATGCAAAAGTGGAGATCCGTGAGTGACACACCGG	1291
Db	1313	TCTAGCTTGGAAATGGAATGCAATGGACATAGAGAAATGGAGATTCGTGAGTGACAGCCCGG	1372
Qy	1292	GAAATCGATCGCAGTGAGCTCAATCCTTAATGGGTCTGGTCACTGTTGGAAGAGCAGCGT	1351
Db	1373	GGACATCAGTTGCAGTGAGCTCAATTTAATGGGTCTAGTCACTGTGGAAGAGCAGCTT	1432
Qy	1352	TCGTCTTTCCGTTATCGTTTCTATCTAACTTAGCCCAAGAGATCAACGCGAAGAAATCA	1411
Db	1433	TTGCTTTCTCTTTCTTTATCAACTTACCAAGAGCATACAGCGGAGAAATCA	1492
Qy	1412	ACTTTAATACATGCAGGTGTGATTTGGTGTCTGGTCTCATGAGAGGTGCTGTATCTATGG	1471
Db	1493	GCATCAAGCAGCAAGTTGTGATCTGTGGGCTGGTCTAATGAGAGGTGCTGTATCTATGG	1552
Qy	1472	CTCTTGATACACAAAGTTTACAGGGCCGGGACACAGATGTACCGGGGAATGCATCA	1531
Db	1553	CTCTTGCGCTACAATAAGTTTACAAGATCAGGACACAGAAATTTGCGCGGGAATGCAATCA	1612
Qy	1532	TGATCAGAGTACGATAAAGTGTCTTTTATAGACAGTGGTGTGTTGGTATGCTGACCA	1591
Db	1613	TGATTACCACTACAATAACCGTCTGTCTTTTATGACACCATGGTGTGTTGGTATGCTAACCA	1672
Qy	1592	AACCATCATAGCTACTATTACCGGACACAGAACGCG-----CACACAGAGCATGT	1642
Db	1673	AACCATCATAGTATAGTAACTTAATGCCACACCAAAAGCGACACAGTACACAGGATGT	1732
Qy	1643	TATCTGATGACAAACCCCAAAATTCATACATATCCTTTGTGG-----ACCAAG	1693
Db	1733	TATCGAGATAGACTCTCGAAATCAATCCATTTCCGCTCTCGATGGTGAACAGCTAG	1792
Qy	1694	ACTGTTCTATGAGCTTTCAGGGAAACCAAAATGTGCTCGGCTGACAGTATACGTGGCT	1753
Db	1793	ATTCAATTTGAGTTTACCTGGGAGCCACAGGAGCTGCGCAGCAACCAACAGCCCTTCGAGGTT	1852
Qy	1754	TCTTTGACAGGCCCACTCGAACCGTGCATTAATCTGAGAGCAATTTGATGACTCTCTCA	1813
Db	1853	TCCTCATGCGCCCAACAGGACTGTCCATTTATCTGAGAGACAGTTTGAATGATGCTCTCA	1912
Qy	1814	TGCGACCCGCTTTTGGAGGTGCTGGCTTTGTATCCCTTTGTTCCAGGTTCTCCAACTGAGA	1873



US-10-424-599-58707  
; Sequence 58707, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 58707  
; LENGTH: 1968  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_24023C.1  
US-10-424-599-58707

Query Match 37.7%; Score 821.8; DB 17; Length 1968;  
Best Local Similarity 70.6%; Pred. No. 9.1e-193;  
Matches 1134; Conservative 0; Mismatches 452; Indels 21; Gaps 2;

QY 292 GATTCTCTAGTGTGAAATGCTTCTGTTATGACATCTGATCAGCGTCTCTGTTGGCG 351  
DB 16 GGTCTCTGTTTCAAAATGCAACGTTATCCACCTCAGACCATGCTCCGTTGGTCTCC 75  
QY 352 TTGATCTCTTGTGTCACCTCTTGTGCTGTATGTTCTTGGTCTATCTTTTGGAAAG 411  
DB 76 ATGAACCTTATTTGGGCACCTCTTGTGGTGTATGTTCTTGGCCATCTCTTGTAGG 135  
QY 412 AATAGATGATGAACCAATCCATCAGCGCTCTGTTGATTTGGCTAGGCACTGTGTACC 471  
DB 136 AATCGGTGATGAACGAGTCTATCAGCTCTTGTGATTTGGTGTGACATGTCATAGTC 195  
QY 472 ATTTGTGTATGATGAAGAAAGCTCGCATCTTCTGCTCTTTAGTGAAGATCTTTTC 531  
DB 196 ATTTGTGTGTTAGTGGTGAAGAAAGCTCGCATATCTTGTGTTTCAAGTGAAGATCTTTTC 255  
QY 532 TTCAATATCTTTTGGCCACCATATATCAATGCGAGGTTTCAAGTGAAGAAAGAGCAG 591  
DB 256 TTATATACCTCTTCAACCATATATTTAATGCCGGTTCAGGTGAAGAAAGAGCAG 315  
QY 592 TTTTTCGCAATTTCTGTGACTATTTATGCTTTTGTGTTGCTTTCGGACTATTTCTTTCG 651  
DB 316 TTTTGTGTTAACTTCATGACCATCATGTTGTTGTTGCTATTTGTTACATTAATCATGT 375  
QY 652 ACAATCATATCTCTAGGTGTAACACAGTCTTTTAAAGATTTGACATTTGGAACCTTTGAC 711  
DB 376 ACCATCATATCTTTGGGTGCCACACAAATTTTAAAGAGTTGGATGTTGCTCTCTGGAA 435  
QY 712 TTGGGTGATATCTTCTATTTGTTGCTATTTGCTGCAACAGATTCAGTATGTACACTG 771  
DB 436 TTAGGGATTTCTTAGCAATTTGTGCAATTTTGTGCAACAGGATTTCTGTTTGCATTTG 495  
QY 772 CAGGTCTCTGAATCAAGACGAGACCTTTGCTTTTACAGTCTTGTATTTGCGAGAGGTTGT 831  
DB 496 CAGGTCTGAATCAGGATGAGACCTTTGCTGTACAGTCTTGTATTTGGGAGGTTGT 555  
QY 832 GTGAATGATGCAACGTCAGTTGTGTTGCTTCAACGCAATTCAGAGCTTTGATCTCACTAC 891  
DB 556 GTGAATGATGCTACATCAGTGTGCTTTTCAATGCAATCAAAAGCTTTGACCTCAACCAA 615  
QY 892 CTAACACGAGCTGCTTTTCTATCTTCTGGAACCTTCTGTTATTTGTTCTCTCACTAGT 951  
DB 616 ATTGACTCTTCAATGCTGTACACTTTTGGGAAATTTCTTGTATCTATTTATTTGAAGC 675  
QY 952 ACCTTGTGTTGGTCTGCAACCGCTCTGATAAGTGTGTTATCAAGAGCTTATCTTT 1011  
DB 676 ACAATGCTGGAGTTTGTGACAGGCTTACTTAGTGCTTACATTTAAGAAAGCTGTACAT 735

QY 1012 GGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTCTTAT 1071  
DB 736 GGCAGGCACTCTACAGATCGTGGGTTGCTCTTATGATGCTTAAATGCACTACCTGCTTAC 795  
QY 1072 ATGCTTGTGAGCTTTTTCGACTTGAGCGGTATCTCTCACTGTGTGTTTCTGTGATTTG 1131  
DB 796 ATGCTTGTGTAATTTATGTTATCTGAGTGGCACTCTCACTGTATTTCTTTTGTGTTGTT 855  
QY 1132 ATGCTCCATTACACATGCGACATGTTAAACGAGAGCTCAAGATATACACAAAGCAATAC 1191  
DB 856 ATGCTCTCATTTATACCTGGCATAAACGTCAGGAGAGTTCAAGAACTACTACCAAGCAATCT 915  
QY 1192 TTTGCAAACTTTGTCAATTTCTTGGGAGACATTTATTTCTTGTATGTTTGGAAATGCAATGCC 1251  
DB 916 TTTGCAAACTTTGTCTTTTGTGCTGAGATCTTTTACTTCTTTTGTGTTGTTGATGCC 975  
QY 1252 TTGGCAATTTGACAGATGGAGATCCGTGATGACACACCGGGAACATGATGATGCAAGTAC 1311  
DB 976 TTGGCAATTTGAAAAATGGAATTTGTGATGATAGCCCTTGAACATCTCTAGCAACTAGT 1035  
QY 1312 TCAATCTTAATGGGTCTGCTCATGTTGGAAGAGAGCGTTCGCTCTTTCCGTTATCGTTT 1371  
DB 1036 TCACTTATTTCTGCTTAATTTCTTGTGAAGAGAGCTTTTGTTCCTTATCTCTTC 1095  
QY 1372 CTATCTAACTTAGCCAAAGAAATCAAAGCGAGAAAAATCAACTTTTAAACATGAGGTTGTG 1431  
DB 1096 ATATCAAACTTGGCTTAAAAAATCAACAAATGAGAAAAATCAGCTTCAGACAGCAAGTATC 1155  
QY 1432 ATTTGGTGTCTGCTCTCATGAGAGGTGCTGATCTATGCTCTTGGCTCTTGCATACAAAGTTT 1491  
DB 1156 ATTTGGTGTGCTGCTCTCATGAGAGGTGCTGTTTCAATGCGCACTTGCATATTAATCAGTTT 1215  
QY 1492 ACAAGGGCGGCGACACAGATGATGACGGGAATCAATCATCATGATCAGGATGAGATAACT 1551  
DB 1216 ACCATGTCGGGCACTCTCTGCGAAGCAATGCAATCATGATCAAGAGCACTTACT 1275  
QY 1552 GTCTGTCTTTTTCAGACAGTGTGTTGTTGATGCTGACCAACCACTCATAGCTTACCTTA 1611  
DB 1276 GTTGTGCTTTTTCAGCACAGTGTGTTGTTGCTGTTGCTTAAAGCACTCATAGGCTTTTA 1335  
QY 1612 TT-----ACCGCACCAAGACCGCACCAAGAGATGTTATCTGATGACAAAC 1659  
DB 1336 CTGCCCCCTACTCCACATCATAAAGAAATCAAGCATCAAGATAATCAAGATCACTACT 1395  
QY 1660 CCAAAATCCATACATATCCCTTTTGTGACCAAGACTCGTTTCAATTGAGCTTTCAGGAA- 1718  
DB 1396 CCAAGTCCAAATCAGTCACTATCCACTTCTTGGGAGTGCCCAAGATCTGAAATTGAT 1455  
QY 1719 -----CCAAATGTCCTCGGCTGACAGATATACGTGCTTCTTGCACGGCCACT 1770  
DB 1456 ATCGATGGCCATGATTTTATCGTCCAAGCAGTATTCGTGCTTCTTACGACTCCAACA 1515  
QY 1771 CGAACCGTGCATTAATCTACTGAGAGCAATTTGATGACTCTTTCATGGAGCCGCTTTTGA 1830  
DB 1516 CACACTGTTCATCGTTTGTGCGTAAAGTTTGTATGATGATTCATGCGCTCTGTTTGTGT 1575  
QY 1831 GGTCTGTGCTTTGTACCTCTTGTTCAGGTTCTTCAACTGAGAGAA 1877  
DB 1576 GGCAGGGGTTTGTCTGTAGAACCTGGCTCACCACCTGAACTGAACTGAACTGAA 1622

RESULT 8  
US-10-369-324-38  
; Sequence 38, Application US/10369324  
; Publication No. US20030221213A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: MENENDEZ-HUMARA, JAIME  
; APPLICANT: YAN, HUA  
; APPLICANT: RICHARD, CRAIG  
; APPLICANT: BRINKERHOFF, W. LEIGH



; PRIOR APPLICATION NUMBER: 60/357,661  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/377,602  
; PRIOR FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 38  
; LENGTH: 1620  
; TYPE: DNA  
; ORGANISM: Solanum tuberosum  
US-10-607-538-38

Query Match 36.6%; Score 797.6; DB 18; Length 1620;  
Best Local Similarity 69.3%; Pred. No. 8.2e-187;  
Matches 1101; Conservative 0; Mismatches 484; Indels 3; Gaps 1;

QY 287 TGTGGATTCCTAGTGTGAACTGCTTGGTATCGACATCTGATCAGCGCTTCTGTGG 346  
DB 11 TGTGGGCTTCTCTGTTTCCAAACTGGGCTCTTTGGGTACTTCAGATCATGCTTCTGTG 70  
QY 347 TTGGGTTGAATCTCTTTGTGCACTTCTTTGTGCTTCTTGTGTTCTTTGGTCACTCTTTGG 406  
DB 71 TATCCATCAACCTCTTTGTGGCACTCTTTGTGCTGTCATCATCATTTGGTCACTCTTTGG 130  
QY 407 AAGAAATAGATGATGAAGAAATCCATCAACCGCTTTTGTGATGGGCTAGGCACTGGTG 466  
DB 131 AGGAAACCGCTGGGTTAATGAGTCCATTAATGCTCCCTCATATAATGGTTGTGTACAGGAG 190  
QY 467 TTACCAATTTGTCATTAAGGAAAGCTCGCATCTTCTGCTTTTGTGAGTCAAGATC 526  
DB 191 TGGTATCTTCTGCTGTAAGTGGTGAAGAACTCACACCTTCTGCTTTTTCAGTGAAGATC 250  
QY 527 TTTTCTTCATATATCTTTTGGCCACCAATTAATTAATGAGGCTTTCAGTGAAGAAAGA 586  
DB 251 TCTTTTTCATATATGTAATCTTCTCCATCATTAATTAATGAGGCTTTCAGTGAAGAAAGA 310  
QY 587 AGCAATTTTCCGCAATTCGTCATTAATGCTTTTGTGCTGTTGTGCACTATTAATTT 646  
DB 311 AGCAATTTTCCGCAATTCGTCATTAATGCTTTTGTGCTGTTGTGCACTATTAATTT 370  
QY 647 CTTCGCAATCATATCTAGTGTGAACAGTCTTTTGAAGAGTTCAGATTTGGAACCT 706  
DB 371 CATGTGCATTAATCATTAAGTGTGAATTCAGATTTTGAAGAGTTCAGATTTGGAATTC 430  
QY 707 TTGACTTGGTGAATATCTTTGCTTAATGCTGCTTATTTGCTGCAACAGATTTCAATGTA 766  
DB 431 TAGATATTGGGATTAATCTTGGCAATTTGAGCAATTTGCTGCCACAGATTCGCTCTGCA 490  
QY 767 CACTGCAAGTTCTGAATCAAGACGAGACACTTTTGTCTTTACAGTCTTTGTAATTCGAGAG 826  
DB 491 CATTGCAAGTCTACATCAGGATGAGACACCCCTCTTTACAGTCTTTGTAATTTGGAGAG 550  
QY 827 GTGTGTGAATGATGCAAGCTGAGTGTGCTTCTCAACGGATTCAGAGTTTGAATCTCA 886  
DB 551 GAGTTGAATGAATGCTACATCGGTGCTTTTCAATGCTATTCAGATTTTGAACCTTGAACCTTA 610  
QY 887 CTCACCTTAAACCAAGCTGCTTTTTCATCTTCTGGAACCTTCTTGAATTTTCTCTCC 946  
DB 611 CGAGGCTGAATCCAGTATAGCCCTCAGTTTCTTGGCACTTCTTATCTGTTCTTTG 670  
QY 947 TAAGTACCTTGTGCTGCAACCGCTCTGATTAAGTGGTGAATTTATCAAGAAGCTAT 1006  
DB 671 CTAGCACTTTACTGGGAGCAGGAAGTGGTCTTCTTAGTCTTACATTAATCAAGAAGCTGT 730  
QY 1007 ACTTTGGAAGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066  
DB 731 ATTTTGGAGCACTCAAGATCTGAGGTGCTTATGATGCTTATGAGTCTGAGGCTTACTTAT 790  
QY 1067 CTTTATATGCTGTGAGCTTTTCCAGTGTGAGCGGTATCTCTCACTGTGTTTTTCTGTGGTA 1126  
DB 791 CATACATGCTGGCTGAATCTTCTATTTGAGTGGGATTTCTCACTGTATTTTCTGTGGTA 850  
QY 1127 TTGTGATGTCCTTACATGTCACATGTAAGGAGAGCTCAAGATTAACAAAGC 1186

## RESULT 10

US-10-369-324-37  
; Sequence 37, Application US/10369324  
; Publication No. US20030221213A1  
; GENERAL INFORMATION:  
; APPLICANT: ROMMENS, CAIUS  
; APPLICANT: YE, JINGSONG  
; APPLICANT: MENENDEZ-HUMARA, JAIME  
; APPLICANT: YAN, HUA  
; APPLICANT: RICHARD, CRAIG  
; APPLICANT: BRINKERHOFF, W. LEIGH  
; APPLICANT: SWORDS, KATHY M. M.  
; TITLE OF INVENTION: PRECISE BREEDING  
; FILE REFERENCE: 058951/0162  
; CURRENT APPLICATION NUMBER: US/10/369,324  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/357,661  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: 60/377,602  
; PRIOR FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 124

DB 851 TTGTAATGCTCTCATTACACTTGGCACAATGTGACCGAGAGTTCAAGAGTCACTACAGGC 910  
QY 1187 ATACCTTTGCAACTTTGTCTATTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATGG 1246  
DB 911 AGCTTTTGGCAACTTTGTCTATTTCTTGGCAGAGACTTTCTCTTCTCTATGTCGGATGG 970  
QY 1247 ATGCCCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGAAACATCGATCGCAG 1306  
DB 971 ATGCTTTGGATATCGAAGAGTGGAAATTTGTTGGTGACAGGCTGGATATCAATTTCCG 1030  
QY 1307 TGAGCTCAATCTCAATTTGGTCTGTCTGTCATGTTTGGAAAGAGCAGGTTCTGCTTTTCCGTTAT 1366  
DB 1031 TGAGTTCAATCTGATGAGGATTAATCTTCTGGGAGAGCTGCTTTGTTGTTTTCATAT 1090  
QY 1367 CGTTTCTATCTAATCTTAGCCAAAGAGAAATCAAGCGAGAAATCACTTTTAACATCGAGG 1426  
DB 1091 CATTTCTTCCAACTTAATGNAAGAAATCTCGGAGCAAAAAATTAACCTTTTGGCAGCAAG 1150  
QY 1427 TTGTGATTTGGTGTCTGTCTCATGAGAGTGTCTATCTATATGCTTGTGATCAACA 1486  
DB 1151 TGATAATATGTTGGGAGGTTTGTGAGAGGCGCAGTGTCCATGGCAGTGGCATATATA 1210  
QY 1487 AGTTTCAAGGCGCGGACACAGATGTACGCGGGAATGCAATCATGATCAGAGTACGA 1546  
DB 1211 AGTTCACTCGTGGGAGACACACTCAACTGCAGGACAAATGCAATTAATGATTACCAGCAGA 1270  
QY 1547 TAACTGTCTGCTTTTGTAGCAGTGGTGTGTTGTTGATGCTGACCAACCACTCATAGCT 1606  
DB 1271 TAACTGTTCTTATTCAGCACAATGTTATCGGTTTAAATGACAAACCCCTTATAAGTC 1330  
QY 1607 ACTTATTAACGACCAAGACGCGCACACAGAGCATGTTATCTGATGACAAACCCCAAAAT 1666  
DB 1331 TCTGCTGCCACACAGAGGCAATTTGAGTACAGTGTCTCATGAGTGCATAATCTCCAAAGT 1390  
QY 1667 CCATACATATCTCTTTTGTGGAC---CAAGACTGTTTCAATGAGCTTTCAGGGAACCA 1723  
DB 1391 CTCCTAACGCCCACTCTCTAGGACGTCGAGAGGACTCTGAAGTTGATTATAATGTTCCAG 1450  
QY 1724 ATGTGCTCGGCTGACAGTATACGTGCTTCTTCACAGCGGCCACTCGAACCGTGCATT 1783  
DB 1451 ATCTTCTCACCACCAAGTTTGAAGATGCTACTTACCGCACCAAGTCAATAAGTGCATC 1510  
QY 1784 ACTACTGGAGACAAATTTGATGACTCTCTTCATCGCACCGCTCTTTGGAGGTCGTGGCTTG 1843  
DB 1511 GGTACTGGCGCAAGTTTGAACGATGCAATTCATCGCCCTATGTTTGGTGGTGGGATTTG 1570  
QY 1844 TACCCTTTGTTCCAGGTTCTTCCAACTGA 1871  
DB 1571 CTCCTCTGCCCTGTTCTTCCAAAGCA 1598



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-369-324-37

Query Match      36.5%; Score 794.4; DB 17; Length 1621;
Best Local Similarity 69.2%; Pred. No. 5.1e-186;
Matches 1099; Conservative 0; Mismatches 486; Indels 3; Gaps 1;

QY 287 TGTGATCTCTAGTGTGAAAGTCCCTTCGTTATCGACATCTGATCAGCTTCTGTGG 346
Db 11 TGTGCTCTCTCTGTTTCCAAAGTGGGCTCTTTGGGTACTTCAGATCATGCTCTCTGTG 70
QY 347 TTGCGTGTGAATCTCTTTTGTGCACTTCTTTGTGCTTGTATTTTGTGTCATCTTTTGG 406
Db 71 TATCCATCAACCTCTTTTGTGGCACTCTTTGTGCTTGTGATCATCATTTGGTCACTCTTGG 130
QY 407 AAGAGATAGATGGATGAACGAATCCATCAACCCCTTGTGTGATGGGCTAGGCACCTGGTG 466
Db 131 AGGAGAACCGCTGGGTAAATAGTCCATTTACTGCCCTCATAAATGGTTGTGTACAGGAG 190
QY 467 TTACCATTTTGTGATTAGTAAAGGAAAGCTCGCATCTTCTGCTTTTAGTGAAGATC 526
Db 191 TGGTTATCTTGTCTCGTAAGTGGTGAAGAGCTCACACCTTCTGCTTTTTCAGTGAAGATC 250
QY 527 TTTTCTTCATATATCTTTTGCACCCATATATTTCAATGCAAGGTTTCAAGTAAAAAAGA 586
Db 251 TCTTTTTCATATATGTTACTTCTTCTTCAATCATATTAATGCAAGGTTTTCAGTAAAAAAGA 310
QY 587 AGCAGTTTTCGCAATTTGCGTGAATTAATGCTTTTGTGCTTTTGTGCACTATTTT 646
Db 311 AGCAATTTTTCGTAAGCTTCAATTAATGATGTTTGGAGCAATGGTACCTGGTCT 370
QY 647 CTGCAATCATCTCTAGTGTGAACAGTCTTCTTAAGAGTTGGACATTTGGAACCT 706
Db 371 CATGTGCCATTAATCATTAAGTGGTCAATTTCAAACTTTCAAGAGTTGGACATTTGGAATTC 430
QY 707 TTGACTTGGTGTATATCTTGTCTTATTTGGTGCATATTTTGTGCAACAGATTTCAAGTATGTA 766
Db 431 TAGATATTTGGGATTAATCTTGCATTTGGAGCATATTTTGTGCAACAGATTTCCGTCTGCA 490
QY 767 CACTGAGGTTCTGAATCAAGACGAGACACCTTTTGTGCTTTTACGTCTGTGATTCGGAGAG 826
Db 491 CATTGCAAGTCTTACATCAGATGAGACACCCCTCTTTACAGTCTTGTATTTGGAGAG 550
QY 827 GTGTTGTGAATGATGCAACGTCTAGTGTGCTTCTCAACGGATTCAGAGCTTTGATCTCA 886
Db 551 GAGTTGTAATGATGATACATCGTGGTGTCTTTTCAATGCTATTTCAAACTTCGACCTTA 610
QY 887 CTCACCTAAACCAACGAGCTGCTTTTTCATCTTCTGAAACTTCTTGTATTTTCTCTCC 946
Db 611 CGAGCATGAATCCAGATAGCCCTCAGTTTCTTGGCAACTTCTTCTATCTGTTCTCTTG 670
QY 947 TAAGTACCTTTGCTGTGCTGCAACCGGTCTGATAAGTGGTATGTTATCAAGAAGCTAT 1006
Db 671 CTAGCACTTTACTGGGAGGAGGAAGTGTCTTCTTAGTGTCTTACATTAATCAAGAAGCTAT 730
QY 1007 ACTTTGGAGGCACTCAACTGACCGAGAGGTGCGCTTATGATGCTTATGGCGTATCTTT 1066
Db 731 ATTTTGGCAGGCACTCCACAGATCGTGAAGTGGTCCCTTATGATGCTCATGGCTTACTTAT 790
QY 1067 CTTATATGCTGTGAGCTTTTTCGATCTGAGCGGTATCCTCACTGTGTTTCTGTGTTA 1126
Db 791 CATACTTGTGCGCGGAATTAATCTATTGAGTGGGATTTCTACCGTCTTTTCTGTGGTA 850
QY 1127 TTGTGATGCCCCATTACATGATGCAATGTTAAGCGAGAGCTCAAGAAATAACAAGC 1186
Db 851 TTGTATGCTCACTACACTTGGCAATGTTGACCGAGAGTTCAGAGTCACTACAAGC 910
QY 1187 ATACCTTTGCACTTTGTCAATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATGG 1246
Db 1187 ATACCTTTGCACTTTGTCAATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATGG 1246
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## RESULT 11

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US-10-607-538-37
; Sequence 37, Application US/10607538
; Publication No. US20040107455A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CATUS
; APPLICANT: YE, JINGSONG
; APPLICANT: HUMARA, JAIME M.
; APPLICANT: YAN, HUA
; APPLICANT: SWORDS, KATHY
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0167
; CURRENT APPLICATION NUMBER: US/10/607,538
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Solanum tuberosum
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US-10-607-538-37

Query Match 36.5%; Score 794.4; DB 18; Length 1621;  
Best Local Similarity 69.2%; Pred. NO. 5.1e-186;  
Matches 1099; Conservative 0; Mismatches 486; Indels 3;

287	QY	TGTTGGATTCTCTAGTGTGAAACATGCGCTTGGTTATCGACATCTGATCAGCTTCTGTGG	346
11	Db		70
347	QY	TTGCGTGTGAATCTCTTTGTTGCACTTTTGTGCTGTGATTGTTCTTGGTCACTTTTGG	406
71	Db		130
407	QY	AAGAGATAGATGGATGAACGAATCCATCAACGCGCTTGTGATGTTGGCTTAGGCATCTGGT	466
131	Db		190
467	QY	TTACCACTTTGTTGATTAGTAAAGAAAGCTGGCACTTCTCGTCTTTTAGTGAAGATC	526
191	Db		250
527	QY	TTTTCTTCATATATCTTTTGGCACCCATATATTCAATGCAGGGTTTCAAGTAAAAAAAGA	586
251	Db		310
587	QY	AGCAGTTTTTCCGCAATTTCTGACTATTATGCTTTTTTGGTGTGTTGGGACTATTATTT	646
311	Db		370
647	QY	CTTGCACAATCATATCTCTAGGTGTACACAGTCTTTTAAAGAGTTGGACATTTGAACT	706
371	Db		430
707	QY	TTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGAGTTCAGTATCTA	766
431	Db		490
767	QY	CATCGAGGTTCTGAAATCAAGAGAGACACTTTTGCTTTTACAGTCTTGTTATTCGAGAGG	826
491	Db		550
827	QY	GTGTTGTGAATGATGCAACGCTCAGTTGTGTCTCAACCGGATTCAGAGCTTTGATCTCA	886
551	Db		610
887	QY	CTCACTAAACCAAGAGCTGCTTTTTCATCTTCTGGAAACTTCTGTATTGTTTCTCC	946
611	Db		670
947	QY	TAAGTACCTTGCTTGGTGTGCAACCGGCTCTGATAAGTGGGTATGTTATCAAGAAGCTAT	1006
671	Db		730
1007	QY	ACTTTGGAAGGCATCTCAACTGACCGAGAGGTTGCGCTTATGATGCTTATGGCGTATCTTT	1066
731	Db		790
1067	QY	CTTATATGCTTGTGAGCTTTTCGACTTGAAGCGGTATCCTCACTGTGTTTTCTGTGCTA	1126
791	Db		850
1127	QY	TTGTGATGCTCCATTACACATGCGACAAATGTAACGGAGAGCTCAGAGATATACAAGAC	1186
851	Db		910
1187	QY	ATACCTTTGCAACTTTGTCTATTTCTTGGCGAGACATTTATTTTCTGTATGTGGAATGG	1246
911	Db		970
1247	QY	ATGCTTTGSAATGTACAAGTGGAGATTCGTTGAGTGACACCGGGAAATCATCGATCGAG	1306
971	Db		1030

Qy	1307	TGAGCTCAATCTCAATGGGTCTGGTCTATGTTTGGAGAGACGCGTTCGTTCCGTTAT	1366
Db	1031	TGAGTTCAATACTACTGAGGACTAATCTTGCTTGGGAGAGCTGCCTTGTGTTTCCATTAT	1090
Qy	1367	CGTTTCTATCTTAAGTTAGCCAAAGAAGNAATCAAAGCGAGAAATCAACTTTAAATCGCAGG	1426
Db	1091	CAITCTTATCCAACTTAATGAAGAAATCTCTGGAGCAAAAATTAACCTTTAGGCAGCAAG	1150
Qy	1427	TTGTGATTTGGTGTCTGTCTCATGAGAGGTGCTGTATCTATGGCTCTTGGCATACAACA	1486
Db	1151	TGATAATATGGTGGCAGGTTTCATGAGAGCGCAGTCTCATGGCACTGGCAATATAATA	1210
Qy	1487	AGTTTACAAGGCGGGGACACAGATGTACGCGGGAATGCAATCATGATCACAGGTACGA	1546
Db	1211	AGTTCACTCGTGGGGACACACTCAACTGCAGGACCAATGCAATAATGATTACCAGCACGA	1270
Qy	1547	TAACTGCTCTCTTTTAGCACAGTGGTGTGGTATGCTGACCAACCACTCATTAAGCT	1606
Db	1271	TAAACCATTTGTTTATTACAGCACAAATGGTATTCGGTTTAATGACAAAACCCCTTATAAGTC	1330
Qy	1607	ACCTATTACCGCACCAAGACGCCACCAACGAGCATGTTATCTGATGACAAACACCCCAAAAT	1666
Db	1331	TCCTGCTGCCACACAGAGGCAATTGAGTACAGTGTCTACGGCGCAATACTCCAAAGT	1390
Qy	1667	CCATACATATCCCTTTGTTGGAC---CAAGACTCGTTTCAATTGAGCCTTCAGGGAACACA	1723
Db	1391	CTCTAACAGACCCCACTCCTAGGCAGTCSAGAGGACTCTGAAAGTTGATTTAAATGTTCCAG	1450
Qy	1724	ATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACAGGCCCACTCGAACCGTGCATT	1783
Db	1451	ATCTTCTCACCCACCAAGTTTGGAGATGCTACTTACCGCAACCAAGTCATAAAGTCATC	1510
Qy	1784	ACTACTGGAGACAATTTGATGACTCTCTCATGCGACCCGCTTTTGGAGGTCGTGGCTTTG	1843
Db	1511	GGTACTGGCGAAGTTTGACATGCATTATGCGCCCTATGTTTGGTGTTCGGGGATTG	1570
Qy	1844	TACCTTTTGTTCAGGTTCTTCCAATGA	1871
Db	1571	CTCCTCTGCCCCCTGGTTCTTCCAACGGA	1598

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RESULT 12
US-10-944-174-1
; Sequence 1, Application US/10944174
; Publication No. US20050032112A1
; GENERAL INFORMATION:
; APPLICANT: Fukuda, Atsunori
; APPLICANT: Tanaka, Yoshiyuki
; TITLE OF INVENTION: Sodium/Proton Antiporter Gene
; FILE REFERENCE: SPO-115C1
; CURRENT APPLICATION NUMBER: US/10/944,174
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US/09/888,035
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: JP 1998-365604
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2330
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (297)..(1901)
; OTHER INFORMATION:
US-10-944-174-1

```

Query Match 35.3%; Score 768.8; DB 19; Length 2330;  
Best Local Similarity 68.6%; Pred. No. 1.4e-179;  
Matches 1077; Conservative 0; Mismatches 487; Indels 6;

1

QY 312 GCCTTGGTATCGACATCTGATCAGCGTCTCTGTGGTGGCTGAATCTCTTTGTCACCT 371  
Db 329 GGCTCTGTACACAGCTCCGACATACCGTGGTGGTGTCCATCAACCTGTGTCTCGCGCT 388  
QY 372 TCTTTGCTGTGATTTCTTGGTCAATCTTTTGGAGAGAAATAGATGGAATCAACATC 431  
Db 389 GCTCTGGGCTGATCGTCTCGGCACCTCTCGAGGAGAAATCGCTGGGTCAATGAGTC 448  
QY 432 CATCACCGCTTGTGATTTGGGCTAGGCACTGTGTGTACCAATTTGTGATTAAGG 491  
Db 449 CATCACCGGCTCATCATCGGCTCTGCAACCGGCTGGTGTCTTCTCATCTACCTCTCCCTCC 508  
QY 492 ABAAGCTCGCATCTTCTGCTCTTGTAGTGAAGATCTTTCTTCATATATCTTTTGGCAC 551  
Db 509 GAAGAGCTCGCATCTTCTGCTCTTGTAGTGAAGATCTTTCTTCATCTACCTCTCCCTCC 568  
QY 552 CATTAATTAATCAATGACAGGTTTCAAGTAAAGAGAGAGTCTTTTCCGCAATTTCTGTAC 611  
Db 569 GATCATCTTCAATGACAGGTTTTCAGGTAAAGAAAGCAATCTTCCGGAAATTTTCATGAC 628  
QY 612 TATTATGCTTTTGGTGTCTGGGACTAATATTCTTTCGACAAATCATATCTCTAGGTGT 671  
Db 629 GATCACATATTGGAGCGCTCGGACAAATGATATCTTTTCACAATATCTATTGCTGC 688  
QY 672 AACACAGTCTTTAAGAGTTGGAGATTTGGAACCTTTGACTTGGGTGATTAATCTGCTAT 731  
Db 689 CATTTGCAATATTACGAGAGATGAACATTTGGAACGCTGGATGTAGAGATTTTCTTCCAA 748  
QY 732 TGGTGCCATATTGCTGCAACAGATTCAGTATGTACACTGCAGGTCTTGAATCAAGACGA 791  
Db 749 TGGAGCCATCTTTCTGCGACAGATTTCTGTCTGCACATTTGCAGGTCTCTCATCAGATGA 808  
QY 792 GACACCTTTGCTTTACAGTCTTGTATTTCGGAGAGGTGTGTGAATGATGCAACGTGAGT 851  
Db 809 GACACCTTTTGTGACAGTCTGTGATTCGTGGAAGGTGTGTGCAACGATGTACATCAAT 868  
QY 852 TGTGCTCTTCAACGCGATTCAGAGCTTTGATCTCACTCACTTAAACCAACGAGCTGCTT 911  
Db 869 TGTGCTTTTCAACGCGATTCAGAGCTTTGATCTTGTCCATAGATGCGGCTGTCTGCTCT 928  
QY 912 TCATCTCTTGGAAACTCTCTGATTTGTTTCTCCTAAGTACCTTCTGCTGGTCTGCAAC 971  
Db 929 GAATTTCTTGGGAACTCTCTTATTATTATTTTGTGAGCACCTCTCTTGGAGTATTGCG 988  
QY 972 CGGCTCTGATAAGTGCATGTATTTATCAAGAGCTATATCTTTGGAAGGCACTCAACTGACCG 1031  
Db 989 TGGATTGCTCAGTGACATATAATCAAGAAGCTATACATTTGGAAGGCAATCTACTGACCG 1048  
QY 1032 AGAGTTGCGCTTATGATGCTTATGGGCTATCTTTCTTATATGCTTGTGCTGAGCTTTTGA 1091  
Db 1049 TGAAGTTGCGCTTATGATGCTATGCGCTTACCTTTTCATATATGCTGGCTGAGTTGCTAGA 1108  
QY 1092 CTTGAGCGGTATCTCAGCTGTGTTTCTGTGGTATTTGTGATGCTCCCATACATGCGCA 1151  
Db 1109 TTTGAGCGGATCTCACCCTATCTCTGTGGTATTTGTAATGTCAATTCACATTCACATTTGGA 1168  
QY 1152 CAATGTAACGGAGAGCTCAAGATAACAACAAGCATACCTTTGCAACTTTTGTCAATTTCT 1211  
Db 1169 TAACGTACAGAGAGTTCAAGAGTTACACAAGACGCAATTTGCAACTCTGTCTCTCAT 1228  
QY 1212 TGGGAGACATTTATTTCTTGTATGTTGGAATGGATGCGCTTGGCAATTCAGTGAAGTGGAG 1271  
Db 1229 TGTGAGACTTTTCTCTCTGCTATGTTGGGATGGATGCAATTTGGAATTTGAAAAATGGGA 1288  
QY 1272 ATCCGTGAGTGACACACCGGACATCGATGCGAGTGAAGTCAATCTTAATGGGTCTGCT 1331  
Db 1289 GTTTGCGAGTGACAGACCTTGGCAATTCATTTGGGATAAGCTCAATTTTGTAGGATTTGT 1348  
QY 1332 CATGTTTGAAGAGACGCTTCTGCTTTTCTGCTTATCTTCTATCTTAACTTTAGCCAAAGAA 1391  
Db 1349 TCTGATTGGAAGAGCTGCTTTTGTATTTCCGCTGTCTGCTTCTGCAACCTTACAAAGAA 1408  
QY 1392 GAATCAAGCGAGAAATCAACTTTTAACATGCAAGTTGTGATTTGGTGGTCTGGTCTCAT 1451

Db 1409 GGACCGAATGAATAAATAAATCTGGAGACAGCAAGTTGTAATATGTTGGCTGGGCTGAT 1468  
QY 1452 GAGAGTGTGTATCTTATGGCTCTTTCATACAAAGATTTTACAAGGGCGGGCACACAGA 1511  
Db 1469 GAGAGAGCTGTGCTGATTGCTCTTGTCTTACAATAAGTTTACAAGATCTGGCCATACTCA 1528  
QY 1512 TGTACCGGGATGCAATCATGATCAGGATAGGATAACTGTCTGCTTTTATAGCACAGT 1571  
Db 1529 GCTGCACGGCAATGCAATTAATGATCACCAGCACCATCACTGTCTGTTCTTTTATAGCACTAT 1588  
QY 1572 GGTGTTTGTATGCTGACCAAACTCACTATAAGTACCTATTACCGCACAGAACGCCAC 1631  
Db 1589 GGTATTTGGATGATGACAAAGCCATTGATCAGGCTGTCTACCGGCTCAGGCCATCC 1648  
QY 1632 CACGAGCATGTTATCTGATGACAAACCCCAAAATCATATATCCCTTTTGTGGACCA 1691  
Db 1649 TGTCACTCTTGTGAGCTTTCATCAAAAGTCCCTGCAATCTCTCTCTCTGCAAG 1702  
QY 1692 AGACTCGTTCATGAGCTTTCAGGAGACCAATGTGCTCGGCTGACAGTATAGTGG 1751  
Db 1703 CATGCAAGGTTCGAGCTTTCAGGAGTACAAACCAATTTGTGAGGCTTCCAGGCTCCGGAT 1762  
QY 1752 CTTCTTTCACACGCGCCCTCGAACCGTGCATTTACTACTGAGACAAATTTGATGACTCTCT 1811  
Db 1763 GCTCTCTCAAGCGACCCACACACTGTCTCACTACTGCGCAAGTTTGCAGCGCGCT 1822  
QY 1812 CATGCGACCGCTCTTTTGGAGGTCTGTGGCTTTGTACCTTTTGTTCAGGTTTCTCAACTGA 1871  
Db 1823 GATGCGCGAGTGTGCGGCGCGGCTTCTGCGGCTTCTCCCTGATCACCAACCGA 1882  
QY 1872 GAGAAACCTCT 1881  
Db 1883 GCAGAGCCAT 1892

## RESULT 13

US-10-155-535-3  
; Sequence 3, Application US/10155535  
; Publication No. US20030046729A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumwald, Eduardo  
; APPLICANT: Apse, Maris  
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY  
; TITLE OF INVENTION: EXPRESSION OF VACUOLAR CATION-PROTON ANTI-PORTERS  
; FILE REFERENCE: 529152000720  
; CURRENT APPLICATION NUMBER: US/10/155,535  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: 09/271,584  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,474  
; PRIOR FILING DATE: 1998-03-18  
; PRIOR APPLICATION NUMBER: 60/116,111  
; PRIOR FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2066  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-155-535-3

Query Match 33.0%; Score 719; DB 14; Length 2066;  
Best Local Similarity 66.0%; Pred. No. 2.9e-167;  
Matches 1056; Conservative 0; Mismatches 540; Indels 3; Gaps 1;  
QY 326 CATCTGATCAGCGCTCTGTGGTGGTGAATCTCTTTGTCACATCTTTTGTGCTTTGTA 385  
Db 50 CTTCTGATCATCATCGGTCTGCTCCATGAATTTGTTCTAGCTTTGCTTTGTGCTTGA 109  
QY 386 TTGTTCTTGGTCACTCTTTTGGAGAGATAGATGATGAACCAATCCATCAGCGCTTGT 445  
Db 110 TCGTCTTGGTCACTTGTCTTGGAGAGACTCGGTGGATGAACGATCAATCACTGCTCTTA 169

446 TGAATGGCTAGGCACTGGTGTACCAATTTTGGTTGATTAGTAAAGGAAAAAGCTCGCATC 505  
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170 TCAATGGTTCGTGTACTGGAGTGTGATCTTGCTTATAAGTGGAGGCAAAAGCTCAAGGA 229  
Qy |||||  
506 TTCTCGCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGGCCACCCATTATATCAATG 565  
Db |||||  
230 TTCTTGTGTTAGTGAAGATCTCTCTTTATTTATCTTCTTCCACCAATTATATCAACG 289  
Qy |||||  
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290 CAGGTTTTCAAGTAAAGAAAGAGCAATTTTTCGCAATTTTCAATGACCAATTATGTTATTG 349  
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350 GTGCTATTGGAACCTCATTTTCAATTTGTTATCATCTCATTTGGTGTAAACATCTTTTCG 409  
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410 AGAAAAATGAAATATCGGTGATCTTACCAATTCGGGACTATCTAGCCATTTGGAGCAATATCT 469  
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470 CTGCTACAGATCTGTTTGCACCTTGCAGGTGCTTAATCAAGACGACGACACCTCTCTTGT 529  
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806 ACAGTCTTTGTTATTCGGAGAGGTTGTTGTAATGATGCAAGCTCAGTTGTGCTCTTCAACG 865  
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1490 CTCGCTCCAGGGCCATTCATCATTACTGGAGGAAATTCGATAACGAGTTATGCGTGGCA 1549  
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1610 CCAATGGAGTCAAGAGTAGAAGAAACAAAGAACG 1648

## RESULT 14

US-10-409-701-22  
; Sequence 22, Application US/10409701  
; Publication No. US200302212241  
; GENERAL INFORMATION:  
; APPLICANT: Zinsmeister, Chris  
; APPLICANT: Helentjaris, Timothy G.  
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress  
; FILE REFERENCE: 1421  
; CURRENT APPLICATION NUMBER: US/10/409,701  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,796  
; PRIOR FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 1638  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1638)  
US-10-409-701-22

Query Match 31.3%; Score 682.6; DB 17; Length 1638;  
Best Local Similarity 65.6%; Pred. No. 2.7e-158;  
Matches 1029; Conservative 0; Mismatches 534; Indels 6; Gaps 2;

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Qy 378 TGTCTGATTTGTTCTTGTGTCATCTTTTGGAAAGAAATAGATGGATGAACGAATCCATCAC 437  
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Qy 438 GCGCTTGTGTTGGGTAGGCACTGGTGTACCATTTTGTGTTAGTATAGTAAAGAAAG 497  
Db GCGCTTGTGTCATGGGCTTCATCACCGGAGGCGTCATCTGCTGTTACTTATATGGGACAA 218  
Qy 498 CTCGATCTCTCTGCTTTAGTGAAGATCTTTTCTTCATATCTTTTTCGCCACCATTTAT 557  
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Qy 978 GATAAGTCCGTATGTTATCAAGAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGTT 1037  
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Qy 1278 GAGTGACACACCGGGAACATCGATTCGAGTCAATCCTAATGGGTCTGCTCATGTT 1337  
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Qy 1578 TGGTATGCTGACCAAACTCATATAAGTACCTATTACCGCACCAAGAGCCACACGAG 1637  
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Qy 1638 CATGTTATCTGATGACAAACCCCAATTCATATATCCCTTTTGGACCAAGACTC 1697  
Db 1582 CGTCGTCTCTGCTCTCAAGCAGTCTATGCTGGACCCACTCTCTTACTAGCATGA ----T 1636  
Qy 1698 GTTCATTTAGCCCTTCAGGGAACCAATGTGCTCGGCTGACAGTATACGTGGCTTCTT 1757  
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Qy 1758 GACACGGCCCACTCGAACCGTGCATTTACTATGAGACAATTTGATGACTCCTTCATGCG 1817  
Db 1697 CACCGCGCCAGCTCGCTCCGCTCCATCGCTTTTGGCGCAAGTTTGAAGATCGGTTTATGCG 1756

Qy 1818 ACCCGTCTTTGGAGGTCTGTGGCTTTTCTACCCTTTGTTCAGGTTCTCCAACTGAGAGAA 1877  
Db 1757 CCGGTGTTTCGGGGGCGAGGTTTCGTCCCTTTGTGCTTGGTTCCCGGTGAGAGAG 1816  
Qy 1878 CCCTCCTGA 1886  
Db 1817 TGTCCCTGA 1825

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Job time : 2810 secs



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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 03:34:19 ; Search time 384 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	821.2	37.7	2553	US-09-830-123-16	Sequence 16, Appl
2	813	37.3	2423	US-09-830-123-14	Sequence 14, Appl
3	774.8	35.6	2237	US-09-830-123-1	Sequence 1, Appl
4	754.4	34.6	2361	US-09-830-123-18	Sequence 18, Appl
5	91.2	4.2	1581	US-09-800-729-22	Sequence 22, Appl
6	64.4	3.0	1354	US-09-800-729-58	Sequence 58, Appl
7	64.4	3.0	1888	US-09-800-729-57	Sequence 57, Appl
8	60.6	2.8	4452	US-09-949-016-849	Sequence 849, Appl
9	59.8	2.7	4460	US-09-949-016-4129	Sequence 4129, Appl
10	53.8	2.5	1291	US-09-524-101D-5	Sequence 5, Appl
11	53.8	2.5	2007	US-08-747-221B-36	Sequence 36, Appl
12	53.8	2.5	2007	US-08-747-221B-38	Sequence 38, Appl
13	53.8	2.5	2007	US-09-005-051-36	Sequence 36, Appl
14	53.8	2.5	2007	US-09-005-051-38	Sequence 38, Appl
15	53.8	2.5	2007	US-09-403-942F-36	Sequence 36, Appl
16	53.8	2.5	2007	US-09-403-942F-38	Sequence 38, Appl
17	53.6	2.5	17612	US-09-949-016-15061	Sequence 15061, A
18	50	2.3	1141	US-09-806-708B-22	Sequence 22, Appl
19	48.8	2.2	1169	US-09-100-391-5	Sequence 5, Appl
20	48.8	2.2	1169	US-09-616-614-5	Sequence 5, Appl
21	48.8	2.2	1302	US-09-100-391-11	Sequence 11, Appl
22	48.8	2.2	1302	US-09-616-614-11	Sequence 11, Appl
23	48.8	2.2	2643	US-09-100-391-9	Sequence 9, Appl
24	48.8	2.2	2643	US-09-616-614-9	Sequence 9, Appl
25	48.4	2.2	684	US-09-248-796A-6653	Sequence 6653, Appl
26	48.4	2.2	1664976	US-08-916-421B-1	Sequence 1, Appl
27	48.4	2.2	1664976	US-09-692-570-1	Sequence 1, Appl

28	47.8	2.2	832	4	US-09-621-976-2813	Sequence 2813, Appl
29	47.6	2.2	915	4	US-09-601-198-7	Sequence 7, Appl
30	46.6	2.1	5852	1	US-07-867-106-2	Sequence 2, Appl
31	46.4	2.1	640681	4	US-09-790-988-1	Sequence 1, Appl
32	46	2.1	505	4	US-09-621-976-15639	Sequence 15639, A
33	46	2.1	3138	1	US-07-867-106-4	Sequence 4, Appl
34	45.4	2.1	1466	3	US-08-984-919A-10	Sequence 10, Appl
35	45.4	2.1	1466	3	US-08-984-919A-12	Sequence 12, Appl
36	45.4	2.1	1472	3	US-08-781-420-10	Sequence 10, Appl
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38	45.4	2.1	1472	3	US-08-874-102-10	Sequence 10, Appl
39	45.4	2.1	1472	3	US-08-874-102-12	Sequence 12, Appl
40	45.4	2.1	1472	3	US-09-006-595A-10	Sequence 10, Appl
41	45.4	2.1	1472	3	US-09-006-595A-12	Sequence 12, Appl
42	45.4	2.1	1875	3	US-08-984-919A-46	Sequence 46, Appl
43	45.4	2.1	1875	3	US-08-984-919A-48	Sequence 48, Appl
44	45.4	2.1	1881	3	US-08-874-102-46	Sequence 46, Appl
45	45.4	2.1	1881	3	US-08-874-102-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1  
US-09-830-123-16  
; Sequence 16, Application US/09830123  
; Patent No. 6803500  
; GENERAL INFORMATION:  
; APPLICANT: Iida, Shigeru  
; APPLICANT: Tanaka, Sachiko  
; APPLICANT: Inagaki, Yoshihide  
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles  
; FILE REFERENCE: 001560-397  
; CURRENT APPLICATION NUMBER: US/09/830,123  
; CURRENT FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: PCT/JP00/05722  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: JP 11/236800  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 2553  
; TYPE: DNA  
; ORGANISM: Nierebergia hybrida  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(2553)  
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles  
; OTHER INFORMATION: pH of vacuoles  
US-09-830-123-16

Query Match	37.7%;	Score	821.2;	DB	4;	Length	2553;	
Best Local Similarity	70.3%;	Pred.	No. 28-199;					
Matches 1115;	Conservative	0;	Mismatches	468;	Indels	3;	Gaps	1;
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QY	529	TTCTTCATATATCTTTTTCGCCACCCATTATTAATCAATGCGAGGGTTTCAAGTAAAAAAGAAG	588					

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QY 1069 TATATGCTGTGAGCTTTTCTGACTGTGAGCGGTATCTCACTGTGTTTCTTGTGTTAT 1128  
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Db 1563 AGCTCAATCTGTCTAGTCTGTTTGGTGGAGGGAGCCCTTGTGTTCCCTTGTCA 1622  
QY 1369 TTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTAAATGAGAGTT 1428  
Db 1623 TTTCTTGTCCAATTTGACCAAGAAATCTGAGGACAGATTTAGCTTTAAACAGAGGTT 1682  
QY 1429 GTGATTTGGTGTCTGCTCATGAGAGTGTGATCTATCTATGCTCTTGTGCAATCAACAG 1488  
Db 1683 ACAATATGGTGGCTGGGCTTATGCGAGGTGCTGTTTCTATGCGCCCTTCTTATAATCAG 1742  
QY 1489 TTTTAAAGGCGCGGCACACAGATGTACCGGGAATGCAATCATGATCACAGTACGATA 1548  
Db 1743 TTTTACAGGGGAGGTCTACTACTAGTTACGTCGAATGCAATTAATGATCACAGTACTATC 1802  
QY 1549 ACTGCTGTCTTTTATGACAGTGGTGTGTTGGTATGCTGACCAAAACCC--ACTCATAGC 1605  
Db 1803 ACTGTTGCTCTTTTACGACAGTGTGTTTGGTGTGATGACAAACCTTTAATCTATTA 1862  
QY 1606 TACCTATTACCGCACAGAACCGGCACACGAGCATGTTATCTGTATGACAAACCCCAAAA 1665

Db 1863 TTGCTACCTCCACAAAAACACITTTGATCAGATGATCTCTCTGAACCGATGACTCCAAAA 1922  
QY 1666 TCATATCATATCCCTTTTGTGGACCAAGACTGTTTCAATTTGAGCTTTCAGGACCAAT 1725  
Db 1923 TCCTTCAATTTGTCCACTTCTTTCAGACACACAAAGACTCAGAACTGATCTGGGCGACAT 1982  
QY 1726 GTGCTTCGCGCTTGACAGTATAGTGGCTTCTTTCAGACGCGCCCACTCGAAACCGTGCAATTAC 1785  
Db 1983 GTACCCCGTCCCCACAGTTTGGGATGCTCTCTGTCACCCCATCTCACACGGTACATTAC 2042  
QY 1786 TACTGAGACAAATTTGATGACTCTCTTCATGCAACCGCTCTTTGGAGTCTGCTGCTTTGTA 1845  
Db 2043 TACTGAGAAAAATTTGACAAATGCAATGCTGCTCTGTTTTCGGTGGACGAGGTTTGTGA 2102  
QY 1846 CCCTTTGTTCCAGGTTCTCCAACTGA 1871  
Db 2103 CCTTTTGTCCAGGATCACCTACTGA 2128

RESULT 2  
US-09-830-123-14  
; Sequence 14, Application US/09830123  
; Patent No. 6803500  
; GENERAL INFORMATION:  
; APPLICANT: Tanaka, Sachiko  
; APPLICANT: Inagaki, Yoshihige  
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles  
; FILE REFERENCE: 001560-397  
; CURRENT APPLICATION NUMBER: US/09/830,123  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: PCT/JP00/05722  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: JP 11/236800  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 2423  
; TYPE: DNA  
; ORGANISM: Petunia hybrida  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2423)  
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the  
; OTHER INFORMATION: pH of vacuoles  
US-09-830-123-14

Query Match 37.3%; Score 813; DB 4; Length 2423;  
Best Local Similarity 70.6%; Pred. No. 2.5e-197;  
Matches 1099; Conservative 0; Mismatches 455; Indels 3; Gaps 1;

QY 318 GTTATCGACATCTGATACCGTTCCTGTGGTGGTGAATCTCTTTTGTGCACTTCTTTG 377  
Db 393 GTTATCGACATCTGATCATCAATCAGTTGTGTCGATAAACTTATTCGTTGCTTATTTG 452  
QY 378 TGCTTGATATCTTCTGCTCATCTTTTGGAGAGATAGATGGAATGGAATCCATCAC 437  
Db 453 CCGGTGATTTGTGATCGGTCATTTTGTGGAAGAAACAGATGGAATGATGATCCATAAC 512  
QY 438 CGCTTGTGATTTGGGCTAGGCATCTGTTTACCATTTTGTGTTAGTAAAGGAAAAAG 497  
Db 513 TGCTTAGTATGTTTCTTCTGTAATGTTATTTCTACTGATAAGTGGAGGAAGAA 572  
QY 498 CTGCAATCTTCTGCTTTTGTAGTGAATCTTTCTTCATATATCTTTTGGCAACCATTTAT 557  
Db 573 CTCTCATATTTTAGTGTTCAGTGAAGATCTTTTCTTCACTTCTTCCGCCAATCAT 632  
QY 558 ATTCAATCGAGGTTTCAAGTAAAGAAAGACAGTTTTTCCGCAATTTTCGTGACTATTAT 617  
Db 633 TTTTATGCTGGTTCAGGTGAAAGAAATCGTTCTTCCGCAATTTTCAGACTATCAT 692  
QY 618 GCTTTTGGTCTGTGGGACTATTATTCTTGTGCAATCATATCTCTAGGTGTAAACA 677

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Db 693 GCTCTTTGGGGCACTTGGGACCTTGTATATCAITTAITATATCAITTAGGTGCCATTGG 752
Qy 678 GTTCTTTAAGAACTTGGACATTTGGAACCTTTGACTTGGGTGATATATCTTCTGCTATTTGGTGC 737
Db 753 CATTTTCAAGAAATGAATATTGGAGCCTTGAATTTGGAGATTACCTTCCAAATGGGGC 812
Qy 738 CATATTTGCTGCAACAGATTCAGTATGTACACTGCGAGGTTCTGAATCAAGACGACACACC 797
Db 813 AATCTTCTCTGTACAGATTTCTGTATGCACCTTACAAGTGTCTTAATCAGGATGAAACACC 872
Qy 798 TTTGCTTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGATGCAACGTCAGTCTTGCT 857
Db 873 CTTATTTGACAGTCTAGTTTTCGGGAAGGTGTGTGAATGATGCCACATCTCTGTAGTTCT 932
Qy 858 CTTCAACGCGATTCAGAGCTTTGATCTCACTCACTAAACCCAGAAAGCTGCTTTTCATCT 917
Db 933 GTTCAATGCTATCCAGACCTTTGACTTATCTACATCGACACGGGCAAGCTATGGAAT 992
Qy 918 TCTTGAAACTTCTGTATTTGTTTCTCTTAAGTACCTTGTCTGGTGTGTCGAACCGGTCT 977
Db 993 AGTTGAAACTTCTTATCTATCTTGTTCCTCAAGCACTGCCCTAGGAGTTGCTGCTGCGCT 1052
Qy 978 GATAAGTGGGTATGTTATCAAGAGCTATATCTTTGGAAGCACTCAACTGACCGGAGGT 1037
Db 1053 ACTGAGCGGCTATATTATTAAGAACTCTACTTTTGAAGGCACCTCAACTGACCGGTGAGGT 1112
Qy 1038 TGCCCTTATGATCTTATGCGGTATCTTCTTATATGCTTGTGAGCTTTTCCACTTTGAG 1097
Db 1113 TGTATTAATGATCTCATGGCTTACCTTACTTACATGCTTGTGTAATTTCTATTTAAG 1172
Qy 1098 CGGTATCTCTACGTGTTTCTGTGATTTGTGATGTCCATTAACACATGACCAATGT 1157
Db 1173 TGCAATCTCTACTGTGTTTCTCTGGGATCGTGTCTCACTACACCTGGCATAATGT 1232
Qy 1158 AACGGAGAGCTCAAGATAACAAAGCATCTCTTGGAGCACTCACTGCACTTCTTCTGGGA 1217
Db 1233 GACTGAGAGCTCGAGAGTCACTACCAAGCACTTTTGTGTACATTAATCAATTTATGCTGA 1292
Qy 1218 GACATTTATTTCTGTATGTTTGGATGATGCTTGGACATTTGCAATGACAGAGATCCGT 1277
Db 1293 AATATTTATATCTTTATGTTGATGATGCTTTGGACATTTGAGAGTGGAAATTTGT 1352
Qy 1278 GAGTGACACACGGGAACATCGATCGAGTGTAGCTCAATCTTAATGGGTCTGTCTATGT 1337
Db 1353 AAGCGACAGCCTTGGAAATACAGTTTCAAGTTAGCTCAATATTCTGGGTCTTCTTTTGT 1412
Qy 1338 TGGAGAGCAGCGTTGCTCTTTCGGTATCGTTTCTATCTAATCTTAGCCAGGAATCA 1397
Db 1413 TGGAGAGCAGCATTTGTTTCCCATTTGCTATCTTGTCCAACTTGACCAAGAAACTCC 1472
Qy 1398 AAGCGAGAAATCAACTTTAAACATGAGGTTGTGATTTGGTGTCTGTCTCATGAGAG 1457
Db 1473 AAGGGGCAAAATTTAGTTTAAACAGCAGGTTACATATGTTGGGTCTGGAATTAAGAGG 1532
Qy 1458 TGCTGTATCTATGGCTCTTGTCATACAAAGTTTACAAGGGCGGGCAGACACAGATGACG 1517
Db 1533 TGCCGTTTCTATGCCCCTTGCTTATATCAAGTTTACAGGGGAGGTCAATCTCAGTTACG 1592
Qy 1518 CGGGAATGCAATCATGATCAGAGTACGATACTGTCTGTCTTTTATGCAAGTGTGTT 1577
Db 1593 CGCAATGCAATTAATGATCAAGATCTATCACTGTGTGCTTTTTCAGCACAGTCTGTGT 1652
Qy 1578 TGTATGCTGACCAACCACTCAT---AAGCTACCTATTACCGCACACAGACGCCAC 1634
Db 1653 TGGTTGATGACAAAACCTTTGATTAAGATATTGCTACCTCTACAAACACTTTGAGCAG 1712
Qy 1635 GAGCATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTTGTGACCAAGA 1694
Db 1713 AATGATCTCTTCTGAACCAAGACCCCAAAATCTTCAATTTGTGCCACTTCTTGCAGCAG 1772
Qy 1695 CTGTTTCAATGAGCCTTTCAGGGAACCACAATGTGCTCTGCGCTTGAAGTATAGTGGCTT 1754
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Db 1773 ACAGACTCAGAAAGCTGATCTGGAAAGCCATGTATACCCGTCGCCAGATTTGCGGATGCT 1832
Qy 1755 CTTGACACGGCCCACTCGAAACCGTGCATTACTACTGGAGACAATTTGATGACTCTTTCAT 1814
Db 1833 CTTTTCAACCCCACTCTACACAGTGCATTTACTGGAGAAAGTTTGACAATGCATTTCAT 1892
Qy 1815 GCGACCCGCTTTTGGAGGTCGTGGCTTTGTACCCTTTTGTCTCCAGGTTCTTCCAACCTGA 1871
Db 1893 GCGTCCAGTTTTCGGTGGAGCGAGGTTTGTACCTTTTGTCTCCAGGATCACCGACAGA 1949

RESULT 3
US-09-830-123-1
; Sequence 1, Application US/09830123
; Patent No. 6803500
; GENERAL INFORMATION:
; APPLICANT: Iida, Shigeru
; APPLICANT: Tanaka, Sachiko
; APPLICANT: Inagaki, Yoshihige
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
; FILE REFERENCE: 001560-397
; CURRENT APPLICATION NUMBER: US/09/830,123
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/JP00/05722
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: JP 11/236800
; PRIOR FILING DATE: 1999-08-24
; NUMBER OF SEQ. ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: Ipomoea nil
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1)..(2237)
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the
; OTHER INFORMATION: pH of vacuoles
US-09-830-123-1
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Query Match 35.6%; Score 774.8; DB 4; Length 2237;
Best Local Similarity 69.2%; Pred. No. 1.3e-187;
Matches 1096; Conservative 0; Mismatches 467; Indels 21; Gaps 2;

Qy 319 TTATCGACATCTGATCAGCGTTCTGTGGTTGGGTGGAATCTCTTTGTGCACTTCTTTGT 378
Db 339 TTGTTCACTGATCATGCTTCCGTTGTGTCGATGAACCTCTTTGTGGCGTTGCTTGC 398
Qy 379 GCTGTATTGTTCTTGGTCACTCTTTTGGAGAGATAGATGGATGAACGNAATCCATCACC 438
Db 399 GCATGCAATGTTCTTGGCCATCTACTCGAGAGAAATCGCTGGGTGAACGNAATCCATTACT 458
Qy 439 GCCTGTTGATGGGCTAGCGACTGCTGTATACATTTTGTGATTAGTAAAGGAAAGAGC 498
Db 459 GCCCTTAATTTGTTTGTGACCGGAGTTGAATTTTGTCTCTTAGCGGAGGAAGAGT 518
Qy 499 TCGCATCTTCTCGTCTTTTAGTGAAGATCTTTTCTTCATATATCTTTTCCACCACCATATA 558
Db 519 TCACATCTTCTCGTCTTTTAGCGAAGATCTTTCTTTATATATCTCTCGCCACCTATAATA 578
Qy 559 TTCATGCAAGGTTTCAAGTAAAGAAAGAGAGTTTTTCGGCAATTTTCGTGACTATTATG 618
Db 579 TTCAATGCGGGGTTTCAAGTAAAGAAAGAGAGTTTTTCGTGAACCTTCAATGACAAATATG 638
Qy 619 CTTTTTGGTGTGGGACTATTATTTCTGCACAATCATATCTCTAGGTGTAACACAG 678
Db 639 CTGTTTGGAGCTATTGGCACACTTATTAGCTGTTCTATTATATCATTTGTGGCGGTCAAA 698
Qy 679 TTCTTTAAGAAAGTTGGACATTTGAACTTTGACTTGGGTGATTTATCTTCTATTGTGTC 738
Db 699 ATTTTCAAGCACTTAGACATTTGACTTTCTGGATTTTGGAGATTTATTAGCAATTTGTGCG 758
Qy 739 ATATTTGTCACAGATTCAGTATGTACACTGCGAGGTTCTGNAATCAAGACGAGACACCT 798
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Db 759 ATATTGCTGCAACCGATCTGTTTGCACATTCAGAGTGTCTCACTCAGGATGAGCGCC 818  
Qy 799 TTGCTTTACAGTCTTGTTATTCGGAGAGGGTCTTGTAATGATGCAAGCTCAGTTGTGGTC 858  
Db 819 CTACTTTACAGTCTGTTGTTGGAGAGGGTCTCAATGATGCTACATCTGTGGTCCCT 878  
Qy 859 TTCAACCGGATTCAGAGCTTTGATCTCACTCACCTAAACCAACGAGCTGCTTTTCAPCTT 918  
Db 879 TTTAATGCTATTCAAGTTTGGACATGACTAGTTTGTGATCCAAAAATTTGGCTTCATTTC 938  
Qy 919 CTGGAACTCTTGTAATTTGTTCTCTAAGTACCTTGCTGTGCTGCTGCAACGGTCTG 978  
Db 939 ATTGGAACCTCTTGTAATTTATTTCTCGAGCACTTTTGGGCGTGGGAATTTGCACTG 998  
Qy 979 ATAAGTCGTATGTTATCAAGAGCTACTTTTGGAGGCACTCAACTGACCCGAGAGTT 1038  
Db 999 CTTTGTGCTATATCAAAAGCTACTTTTGGAGGCACTCAACGATCGTAGGTT 1058  
Qy 1039 GCCCTTATGATGCTTATGGGCTATCTTTCTATATGCTTCTGAGCTTTTCGACTTGAGC 1098  
Db 1059 GCCCTTATGATGCTATGCTTCTTCTTATATATGCTTCTGAGTTTATCTATCAAGC 1118  
Qy 1099 GGTATCTCTACTGTTTCTGCTGTTATGCTGATGCTCCATTTACATGCGCAATGTA 1158  
Db 1119 GGCATCTTACTGTATTTCTGTGGAATTTGTATGCTCTCAATTAACCTGCGCAATGTT 1178  
Qy 1159 ACGGAGAGCTCAAGATAACAAAGCATACCTTTTGCACCTTTTGCACTTTCTTGGGAG 1218  
Db 1179 ACGGAGAGCTCAAGGTCATCTAGGCATCTCTTGGCACTCTGCTATTTGTGGAGAG 1238  
Qy 1219 ACATTTATTTCTTGTATGTTGAATGATGCTTGGACATTCAGAGTGGAGATCCGTG 1278  
Db 1239 ACATTTATCTCTCTATGTTGTTGATGATGCTTGGATATCGAGAAATGGAATTTTG 1298  
Qy 1279 AGTGACACCGGAGACATCGATCGCAGTCACTCAATCTAATGGTCTGGTCTGATGGTT 1338  
Db 1299 AAAAATAGTCAGGACATCAGTTGTCAGTCAATATTTGTAGCGCTTAATCTTAGTA 1358  
Qy 1339 GGAAGAGCAGCTTCTGCTTTCGTTTATCGTTTCTATCTAATCTAGCAAGAGATCAA 1398  
Db 1359 GGCAGAGCTGGTTCGTTATTTCCCTTGTCTGTTTATCCAACTCTGCTATTTGTGGAG 1418  
Qy 1399 AGCGAGAAATCAACTTTAATGCTGAGTGTGATTTGGTGTCTCTCATGAGAGT 1458  
Db 1419 TCGGACAAAGATATCTTTAGGCAACAAATAAATTTTGGTGGCTGGCTTAATGAGAGC 1478  
Qy 1459 GCTGTATCTATGCTCTTGATCAACAGTTTACAGGGCCGGGCGACACAGATGTACGC 1518  
Db 1479 GCCGTCTCAATAGCATTGGTATATAAGTTTACAACTTCGGGGCATACGTCATTGGAC 1538  
Qy 1519 GGAATGCAATCATGATCAGAGTACGATAAATCTGCTGCTTTTATAGCACAGTGGTGT 1578  
Db 1539 GAGAACCAATATGATTACAAGTACTGTTACGGTTGTTCTGTTACAGCAGTGTATTTC 1598  
Qy 1579 GGTATGCTGACCAACCACTCATAGAGTACTTATTCAGGACCAAGAGCCGACACGAGC 1638  
Db 1599 GGGTTGATGACGAAGCTCTGTATAAACCTTCTGCTACCCCGCACAAAGCAGATGCCAAGC 1658  
Qy 1639 -----ATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTG 1683  
Db 1659 GGTCAATTCATGACAACTCCGAACCCAGTAGTCCGAAGCATTACGGTGGCCACTC 1718  
Qy 1684 TTGGACCAA-----GACTCGTTTCAATTGAGCCCTTCAGGGAACCAAAATGTGCTCGGCT 1737  
Db 1719 CTGGACAAACCAACCTGACTCAGAAACGATATGATAACCGGACCTGAGGTGTCTGACCA 1778  
Qy 1738 GACAGTATAGTGGCTCTTTGACACGGCCCACTCGAAGCGTGGATTACTACTGGAGACAA 1797  
Db 1779 ACTGCCCTGGCATGCTGCTAAGGACGCCCAACCCACACCGTGCACCGCTACTGGGCTAG 1838  
Qy 1798 TTTGATGACTCTCTCATGCGACCGCTTTTGGAGGTCGTGGCTTTGTACCCCTTTGTTC 1857

Db 1839 TTTGATGATTCGTTTATGGTCCCGTGTGTTGGCGGGGATTCGTTCCGTTGTGCGC 1898  
Qy 1858 GGTTCCTCCAACTCAGAGAAACCT 1881  
Db 1899 GGCTCCACAGTTGAGCAGAGCCCT 1922  
RESULT 4  
US-09-830-123-18  
; Sequence 18, Application US/09830123  
; Patent No. 6803500  
; GENERAL INFORMATION:  
; APPLICANT: Iida, Shigeru  
; APPLICANT: Tanaka, Sachiko  
; APPLICANT: Inagaki, Yoshihide  
; TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles  
; FILE REFERENCE: 001560-397  
; CURRENT APPLICATION NUMBER: US/09/830,123  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: PCT/JP00/05722  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: JP 11/236800  
; PRIOR FILING DATE: 1999-08-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 2361  
; TYPE: DNA  
; ORGANISM: Torenia hybrida  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(2361)  
; OTHER INFORMATION: Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles  
US-09-830-123-18  
Query Match 34.6%; Score 754.4; DB 4; Length 2361;  
Best Local Similarity 68.4%; Pred. No. 2,2e-182;  
Matches 1090; Conservative 0; Mismatches 471; Indels 33; Gaps 2;  
Qy 319 TTATCGACATCTGATCAGCTTCTGCTGTTGGTGGTGGATCTCTTTGTTGCACTTCTTGT 378  
Db 444 TTGTGGAGCTCTGTGCAGGTTTCAGTGTGCGGTATAAATCTTATTTGTCACTTCTCTG 503  
Qy 379 GCTTGTATTTCTTGGTCACTCTTTTGAAGAGATAGATGATGAACAAATCCATCACC 438  
Db 504 ACACTATAGTATGTTGTTCACTCTCTGAGGAAACCTTGGATGAATGATCTATCAT 563  
Qy 439 GCTTGTGATGGCTAGGCACTGCTGTACCAATTTTGTGATTTAGTAAAGGAAAAAGC 498  
Db 564 GCCCTCATAATTTGTTAGCCACGGGAGTTATAATCTCTGTTAATAGTGGTGAAGAAC 623  
Qy 499 TCGCATCTCTGCTCTTTAGTGAAGATCTTTCTTCATATATCTTTTGGCACCATTATA 558  
Db 624 TCCCATCTCTTGGTGTTCAGTGAGATCTTTTCTTCATCTATGCGCTGCCACCAATCAT 683  
Qy 559 TTCAATGACAGGTTTCAAGTAAAGAAAGCAGTGTTCGCAATTTCTGTCATATTATG 618  
Db 684 TTTAATGCGGGTTCAGTAAGTAAGAAATCAATCTTTTCGCAATTTGCAACTATATG 743  
Qy 619 CTTTTTGTGCTGTTGGGACTATTATTTCTTGCAATCATCTCTAGGTGTAAACAG 678  
Db 744 ATGTTTGGAGCAGTTGGTACCTTGATATCTTCATCATCAITTCACCTCGTACCAATTGA 803  
Qy 679 TTTTAAAGAGTTGGACATTTGGACCTTTGACCTTTGGGTGATTAATCTGCTATTGGTCC 738  
Db 804 TTTTCCCAAAATGAACATGAGA---CTTGGAGTTGGAGATTATCTTCTGCTATTGGAGCT 860  
Qy 739 ATATTGCTGCAACAGATTCATGATGTACACTGCGAGTTCTGAATCAAGAGGACACCT 798  
Db 861 ATTTTGTGCAACAGACTCAGTTTGCACATACAGGTGCTAAGCCAGGACGAAACCA 920  
Qy 799 TTGCTTTACAGTCTTGTATTTCGGAGAGGGTGTGTGTAATGATGCAACGTCAGTTGTGTC 858



Db 913 GACTGGTGTGTGACTGCTCVAGTGACTAAGTTTACAAACGACACGCTTTCCCTGCT 972  
Qy 1032 AGAGTTGCCCTTATGATGCTTATGGGTATCTTTCTTATATGCTTGTGAGCTTTTCGA 1091  
Db 973 GGAGACGGCGTGTCTTCTCATGTCTGGAGCAGCTTCTCTTGCGAGAGCTCGG 1032  
Qy 1092 CTTGAGCGGTATCCTCACTGTGTTTCTGTGGTATGTTGATGTCCTCATACATGGCA 1151  
Db 1033 ATTTACAGGTGTGTAGTGTCTTCTTCTGGAATCACACAAGCTCATACACCTACA 1092  
Qy 1152 CAATGTAACGGAGAGCTCAGATAACAACAAGACATACCTTTGCACTTTGTCTTCT 1211  
Db 1093 CAATCTCTGCGTGAATCAAGAAGTCGAACAAGCAGCTCTTTGAGGTGTACATTTCT 1152  
Qy 1212 TCGGAGACATTTATTTCTTGTATGTTGGAATGATGCTTGGACATTCACAAG 1266  
Db 1153 GCGAGAGAACTTCACTTCTCTACATGGCGCTGGCACTGTTACCTTCCAGAG 1207

## RESULT 6

US-09-800-729-58  
; Sequence 58, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: NI et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 1354  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-800-729-58

Query Match 3.0%; Score 64.4; DB 4; Length 1354;  
Best Local Similarity 54.7%; Pred. No. 2.5e-06;  
Matches 128; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 1033 GAGTTGCCCTTATGATGCTTATGGGTATCTTTCTTATATGCTTGTGAGCTTTTCGAC 1092  
Db 18 GAGACGGCGTGTCTTCTCATGTCTGGAGCAGCTTCTCTTGCGAGAGCTCGGGA 77  
Qy 1093 TTGAGCGGTATCCTCACTGTGTTTCTGTGGTATGTTGATGTCCTCATACATGGCA 1152  
Db 78 TTTACAGGTGTGTAGTGTCTTCTTCTGGAATCACACAAGCTCATACACCTACAAC 137  
Qy 1153 AATGTAACGGAGAGCTCAGATAACAACAAGACATACCTTTGCACTTTGTCTTCTT 1212  
Db 138 AATCTGTGCGTGAATCAAGAAGTCGAACAAGCAGCTCTTTGAGGTGTACATTTCTG 197  
Qy 1213 GCGGAGACATTTATTTCTTGTATGTTGGAATGATGCTTGGACATTCACAAG 1266  
Db 198 GCGAGAGAACTTCACTTCTCTACATGGCGCTGGCACTGTTACCTTCCAGAG 251

## RESULT 7

US-09-800-729-57  
; Sequence 57, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: NI et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800,729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013

; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 1688  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (21)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (69)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (99)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-800-729-57

Query Match 3.0%; Score 64.4; DB 4; Length 1688;  
Best Local Similarity 54.7%; Pred. No. 2.7e-06;  
Matches 128; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 1033 GAGTTGCCCTTATGATGCTTATGGGTATCTTTCTTATATGCTTGTGAGCTTTTCGAC 1092  
Db 345 GAGACGGCGTGTCTTCTCATGTCTGGAGCAGCTTCTCTTGCGAGAGCTCGGGA 404  
Qy 1093 TTGAGCGGTATCCTCACTGTGTTTCTGTGGTATGTTGATGTCCTCATACATGGCA 1152  
Db 405 TTTACAGGTGTGTAGTGTCTTCTTCTGGAATCACACAAGCTCATACACCTACAAC 464  
Qy 1153 AATGTAACGGAGAGCTCAGATAACAACAAGACATACCTTTGCACTTTGTCTTCTT 1212  
Db 465 AATCTGTGCGTGAATCAAGAAGTCGAACAAGCAGCTCTTTGAGGTGTACATTTCTG 524  
Qy 1213 GCGGAGACATTTATTTCTTGTATGTTGGAATGATGCTTGGACATTCACAAG 1266  
Db 525 GCGAGAGAACTTCACTTCTCTACATGGCGCTGGCACTGTTACCTTCCAGAG 578

## RESULT 8

US-09-949-016-849  
; Sequence 849, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 849  
; LENGTH: 4452  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-849

Query Match 2.8%; Score 60.6; DB 4; Length 4452;  
Best Local Similarity 47.7%; Pred. No. 3.8e-05;  
Matches 365; Conservative 0; Mismatches 364; Indels 36; Gaps 5;

Qy 514 TTTAGTGAAGATCTTTCTTCTCATATATCTTTTGGCCCATATATCAATGACAGGTTT 573



471	TTTGATCGAGAGTATTTTTTCAACATATATTACTTCTCTATCATATTTTATGCGAGTTAT	530
574	CAAGTAAAAAGAACGAGTTTTTCGCGCAATTTCTGACTATTTATGACTTTTTTGGTCTGTT	633
531	AGCTGAAAGGAGACATTTTTTTTTCGAAATCTTGGGTCTATCTCTAGCATACGCTTTTCTT	590
634	GGNCTATTATTTCTTGCA-----CAATCATATCTCTAGGTGTAAACAGATTC	681
591	GGAAACGCAATTTCTTGTTCGTTATTGGGTCAATAATGTATGGCTGTGTAAACGCTGATG	650
682	TTTAAAGAGTTGGACATT--GGAACCTTTGCACTTGGGTGATTATCTTGTATTCTGTGCC	738
651	AAGGTAAAGGAGCACTTTCGAGGAGATTTTTTACATTTACAGATGCTACTGTTTGGTGCC	710
739	ATATTTTCTGCAACAGAGATTCAGTATGTACACTGCGAGTTTCTGAATCAAGACGAGACACT	798
711	ATTGATACGAACTGTATCCAGTCTTCTGCTATATCCACGAGCTTCAAGTTGAT	770
799	TTG---CTTTACAGTCTTGATTCGGAGAGGGTGTGTGAATGATGCAACGTCAGTTGTG	855
771	GTTGAACTCTATGCACTCTTTTTTGGTGAAGAGTGTCTCAATGATGCTGTGGCCATAGTG	830
856	GTCTTCAACGGGATTCAGAGCTTTGATCTCACTCACCTAAAC-----CAC	900
831	CTGTCTCTCTCAATGATGGGCATACCAGCAGCTGGAGACACAGTCACACCTTTTGATGTC	890
901	GAAGCTGCTTTTCATCTTTTGGAAACTTCTTGTTATTTGTTTCTCTAAGTACCTTGTCT	960
891	ACAGCGATGTTCAAGTCTATTGGGATCTTCTTGGNATCTTCAGTGGATCTTTTGCATG	950
961	GGTGCTGCAACCGGTCTGATAAAGTGCGTATGTATCAAGAAGCTATATCTTTGGAAAGCAC	1020
951	GGTGCTGCTACTCGAGTGGTGACAGCTTTAGTGACAAAGTTTCAACCAAT---ACGGAG	1007
1021	TCAACTGACCGAGAGGTTGCCCTTATGATAGCTTATGCGGTATCTTTCTTTATATGCTTGT	1080
1008	TTCCAGTTGTTGGAGACAGGCGCTGTTCTTCTTGATGTCCTCGAGTACCTTCTCTTGGCT	1067
1081	GAGCTTTTCGACTTTGAGCGGTATCCTCACTGTTTTTCTGTGGTATTGTGATGTCCTCAT	1140
1068	GAAGCATGGGCGCTTCACAGGTGTAGTGCAGTATGTTTTTGTGGCATCACACGACAT	1127
1141	TACACATGGCACAATGTAAACGGAGAGCTCAAGAATAACAAAGCATACCTTTTGCACCT	1200
1128	TATACGTTAATAATTTGTCACGGAGTCTCAGCATAGAACTAAACAGTTGTTTGAGCTT	1187
1201	TTGTCAATTTCTGCGGAGACATTTATTTTCTTTGTATGTTGGAATG	1245
1188	CTCAATTTCTGGCAGAGAAATTCATCTTCTCTCCACATGGGCGTG	1232

RESULT 9

```

RES001.3
US-09-949-016-4129
; Sequence 4129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4129
; LENGTH: 4460
; TYPE: DNA

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DEC 10 1961

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RESOLUTION 10
US-09-524-101D-5
; Sequence 5, Application US/09524101D
; Patent No. 6762291
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: INSECT P53 TUMOR SUPPRESSOR GENES AND PROTEINS
; FILE REFERENCE: EX00015C FIRST AMENDMENT
; CURRENT APPLICATION NUMBER: US/09/524,101D
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 09/268,969
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: US 60/184,373

```





RESULT 15  
US-09-403-942F-36  
; Sequence 36, Application US/09403942F  
; Patent No. 6664090  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary M.  
; APPLICANT: Brandt, Kevin S.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: NOVEL CARBOXYLESTERASE NUCLEIC ACID MOLECULES, PROTEINS AND USES  
; FILE REFERENCE: FC-1-CI-PUS  
; CURRENT APPLICATION NUMBER: US/09/403,942F  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US97/20598  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 08/747,221  
; PRIOR FILING DATE: 1996-11-12  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 2007  
; TYPE: DNA  
; ORGANISM: Ctenocephalides felis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (11)..(1594)  
; OTHER INFORMATION:  
US-09-403-942F-36

Query Match 2.5%; Score 53.8; DB 4; Length 2007;  
Best Local Similarity 52.4%; Pred. No. 0.0015;  
Matches 118; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy	1954	AAATTATGCTTTTGTGTAATTTATCCATTTTGTATATTTGTTGTGAGGACAGAAATCTGT	2013
Db	1775	ACAAATTCGTGTTTGTGATTTGCGCATTTCAACAGATGGTGTACTGTGCGCTAAATTTGT	1834
Qy	2014	CCTAACGTTTGTGAGAGCAGAAAGCAAAACATGGCACTTTGAAGTGTGTTGATTGATGTAT	2073
Db	1835	CGCTCTTCTTGAAGAAGCTGAACATAAATGATTAATGACGCCACATTTATATTT	1894
Qy	2074	GTAATATATTCATATTTGTTGTTGTAACACAACTACACATTTGTTTATGTTTGGAA	2133
Db	1895	GATATTAATACCATCTTTGTATCATATTTGCTTTTATTTTTCATTTTTTTATTCA	1954
Qy	2134	TTTGGTTTCTTCGAAAAAATAAAAAAAAAAAAAAAAAAAAAA	2178
Db	1955	AATATATGTTTTTTTATATAAAAAAAAAAAAAAAAAAAAAA	1999

Search completed: April 26, 2005, 08:45:17  
Job time : 396 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 02:22:21 ; Search time 1194 Seconds  
(without alignments)  
10798.322 Million cell updates/sec

Title: US-10-617-623-1

Perfect score: 2178

Sequence: 1 cctctgttcttctctcg.....aaaaaaaaaaaaaaaaaaaaa 2178

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2178	100.0	2178	2	Aaz22591 Arabidops
2	2143.4	98.4	2284	2	Aaz22595 Arabidops
3	1617	74.2	1617	6	Abz13434 Arabidops
4	1617	74.2	1617	12	Adh74230 Thale cre
5	1614	74.1	1614	12	Adnl1979 Wild type
6	1612.4	74.0	1614	12	Adnl1981 Atnhx1 mu
7	1563	71.8	1563	12	Adnl1983 Atnhx1 mu
8	1563	71.8	1566	12	Adnl1989 NDL-1 enc
9	1473	67.6	1473	12	Adnl1985 Atnhx1 mu
10	1407	64.6	1410	12	Adnl1991 NDL-2 enc
11	1362	62.5	1362	12	Adnl1987 Atnhx1 mu
12	1320.4	60.6	1323	12	Adnl1993 NDL-3 enc
13	848	38.9	1449	12	Adm68265 Plant Na+
14	832.8	38.2	1668	3	Aaa72926 Atliplex
15	821.2	37.7	2553	4	Aaf75765 Gene regu
16	813	37.3	2423	4	Aaf75764 Gene regu
17	806.4	37.0	1668	6	Acc49921 Suaeda sa
18	806.4	37.0	2397	6	Acc49920 Suaeda sa
19	805.4	37.0	1315	12	Adm68266 Arabidops
20	797.6	36.6	1620	10	Adj99891 Potato sa

21	794.4	36.5	1621	10	Adj99890 Potato sa
22	774.8	35.6	2237	4	Aaf75752 Gene regu
23	768.8	35.3	2330	3	Aaa61876 cDNA enco
24	754.4	34.6	2361	4	Aaf75766 Gene regu
25	682.6	31.3	1638	10	ACF58165 2. may8 s
26	651	29.9	1955	11	Adm82830 Agropyron
27	523.8	24.0	1788	2	Aaz22592 Arabidops
28	491.6	22.6	1674	6	Abk12638 DNA enco
29	418	19.2	418	8	Abx62293 Arabidops
30	401.8	18.4	1740	12	Adm68263 Mangrove
31	269.2	12.4	612	13	ACN53419 Cotton an
32	252.6	11.6	330	2	Aaz22611 Arabidops
33	226.4	10.4	378	2	Aaz22606 Rice Na/H
34	191	8.8	613	10	Adl17688 DNA (Seq1
35	165.2	7.6	466	12	ADP94869 Cotton ex
36	165.2	7.6	466	13	ADR62082 Cotton cD
37	153.2	7.0	588	10	ADD17689 DNA (Seq1
38	152.2	7.0	573	13	ACN47580 Cotton pr
39	149.4	6.9	596	13	ACN60354 Cotton gy
40	146.4	6.7	2000	6	ABz16128 Arabidops
41	141.8	6.5	1824	3	AAC95373 Cat flea
42	141.8	6.5	1824	3	AAC95372 Cat flea
43	141.8	6.5	2080	3	AAC95370 Cat flea
44	141.8	6.5	2080	3	AAC95371 Cat flea
45	125	5.7	281	6	ABL73323 Corn tass

#### ALIGNMENTS

#### RESULT 1

Aaz22591

ID Aaz22591 standard; cDNA; 2178 BP.

XX AAZ22591;

DT 18-JAN-2000 (first entry)

DE Arabidopsis thaliana Na/H transporter gene AtNHX1.

XX Sodium; proton; antiport; transporter; salt tolerance; salt management;  
KW transgenic plant; survival; soil; farming; accumulation; irrigation;  
KW crop; ss.

XX Arabidopsis thaliana.

PN WO9947679-A2.

XX 23-SEP-1999.

PF 18-MAR-1999; 99WO-CA000219.

PR 18-MAR-1998; 98US-0078474P.

PR 15-JAN-1999; 99US-0116111P.

XX (BLUM/) BLUMWALD E.

PA (APSE/) APSE M.

PA (SNED/) SNEDDEN W.

PA (AHAR/) AHARON G.

XX Blumwald E.; Apse M, Snedden W, Aharon G;

XX WPI; 1999-571840/48.

XX P-PSDB; AAY40901.

XX Nucleic acid molecules encoding sodium/proton transport polypeptides,  
XX useful in genetic engineering salt tolerance in crop plants.

XX Claim 4; Fig 1A; 93pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a  
XX plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and  
XX capable of increasing salt tolerance in a cell. This sequence corresponds

CC to the gene encoding the AtNHX1 transporter from *Arabidopsis thaliana*.  
 CC The Na/H transporter polypeptides provide a means of intracellular salt  
 CC management, particularly in plants. The sequences are useful for  
 CC producing transgenic plants that are capable of surviving in soil with  
 CC high salt levels that would normally inhibit growth of the crop species.  
 CC This would be useful in farming land in areas that are generally  
 CC considered unproductive through salt accumulation and poor irrigation,  
 CC e.g. in India, Australia, and prairies in USA or Canada. Commercial  
 CC crops, such as potatoes, tomatoes, brassica, cotton, sunflower,  
 CC strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley,  
 CC atriplex, sorghum, alfalfa, salicornia and others would benefit from  
 CC increased salt tolerance  
 XX

SQ Sequence 2178 BP; 576 A; 413 C; 472 G; 717 T; 0 U; 0 Other;

Query Match	100.0%;	Score 2178;	DB 2;	Length 2178;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2178;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	CCTCTGTTTCGTTCTCTGTTAGTGAAGAAAGAAAGAAATCTCAGGTTTTCGGA	60		
Db 1	CCTCTGTTTCGTTCTCTGTTAGTGAAGAAAGAAAGAAATCTCAGGTTTTCGGA	60		
Qy 61	AGCTTCCAAAATTTTGAATTTGATCTCTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT	120		
Db 61	AGCTTCCAAAATTTTGAATTTGATCTCTCTGGGCTCTTTTGTAAATCAGACTGAAGATAT	120		
Qy 121	TTAGATTACCCAGAAAGTTGTTCAAGGAAATGTTTTCAGTGACAGCAGCGAAAGATAAAG	180		
Db 121	TTAGATTACCCAGAAAGTTGTTCAAGGAAATGTTTTCAGTGACAGCAGCGAAAGATAAAG	180		
Qy 181	AGACTTTTTCCTCAGATTTTTCGATCCAAAATCTGAATAGTTGTTTCATGTTCTTGGAT	240		
Db 181	AGACTTTTTCCTCAGATTTTTCGATCCAAAATCTGAATAGTTGTTTCATGTTCTTGGAT	240		
Qy 241	CAAACTGGAAAGGAGGTTTCTGATCTAGATCTAGAAAGATAAATTTGGATTTCTTA	300		
Db 241	CAAACTGGAAAGGAGGTTTCTGATCTAGATCTAGAAAGATAAATTTGGATTTCTTA	300		
Qy 301	GTGTGCAAAATCGCTTCTGATCTGATCTGATCTGCTTCTGTTGCTGTTGAATCTC	360		
Db 301	GTGTGCAAAATCGCTTCTGATCTGATCTGATCTGCTTCTGTTGCTGTTGAATCTC	360		
Qy 361	TTTGTGTCATCTCTTGTGCTGTAATGTTTCTTGGTCACTCTTTTGAAGAAGATAGATG	420		
Db 361	TTTGTGTCATCTCTTGTGCTGTAATGTTTCTTGGTCACTCTTTTGAAGAAGATAGATG	420		
Qy 421	ATGAACGAATCCATCAACCGCTTGTGATTTGGCTAGGCACTGCTGTACCATTTTGTG	480		
Db 421	ATGAACGAATCCATCAACCGCTTGTGATTTGGCTAGGCACTGCTGTACCATTTTGTG	480		
Qy 481	ATTAGTAAAGGAAAGCTCGCATCTTCTGCTTTTGTAGTGAAGATCTTTTCTCATATAT	540		
Db 481	ATTAGTAAAGGAAAGCTCGCATCTTCTGCTTTTGTAGTGAAGATCTTTTCTCATATAT	540		
Qy 541	CTTTTGGCCACCAATTAATTAATCAATGAGGTTTCAAGTAAAGAAAGAGAGTTTTCGCG	600		
Db 541	CTTTTGGCCACCAATTAATTAATCAATGAGGTTTCAAGTAAAGAAAGAGAGTTTTCGCG	600		
Qy 601	AAATTCGTGACTAATTAATGCTTTTGTGCTTTGTTGGGACTATTATTTCTTTGCAATCATAT	660		
Db 601	AAATTCGTGACTAATTAATGCTTTTGTGCTTTGTTGGGACTATTATTTCTTTGCAATCATAT	660		
Qy 661	TCCTTAGGTGTAAACAGATTCTTTAAGAAAGTTGGAATTTGGAACCTTTTGAATTTGGTGTAT	720		
Db 661	TCCTTAGGTGTAAACAGATTCTTTAAGAAAGTTGGAATTTGGAACCTTTTGAATTTGGTGTAT	720		
Qy 721	TATCTTGTCTATTTGGTGGCAATTTTGTGCAACAGATTCAATGATGATGATGATGATGATG	780		
Db 721	TATCTTGTCTATTTGGTGGCAATTTTGTGCAACAGATTCAATGATGATGATGATGATGATG	780		
Qy 781	AATCAAGACGAGACACTTTTGTCTTACAGTCTTGTATTCGAGAGGTTTCTGTGAATGAT	840		
Db 781	AATCAAGACGAGACACTTTTGTCTTACAGTCTTGTATTCGAGAGGTTTCTGTGAATGAT	840		

Db	781	AATCAAGACGAGACACTTTTGTCTTACAGTCTTGTATTCGAGAGGTTTCTGTGAATGAT	840
Qy	841	GCACCTCAGTTTGTGTCTTCAACGGGATTCAGAGCTTTGATCTCACTCACTAAACCCAC	900
Db	841	GCACCTCAGTTTGTGTCTTCAACGGGATTCAGAGCTTTGATCTCACTCACTAAACCCAC	900
Qy	901	GAAGCTGCTTTTCACTCTCTCGAAACTTCTTGATTTCTTCTCTTAAGTACCTTGTCTT	960
Db	901	GAAGCTGCTTTTCACTCTCTCGAAACTTCTTGATTTCTTCTCTTAAGTACCTTGTCTT	960
Qy	961	GGTGTGCAACCGGCTGATTAAGTGGTATGTTATCAAGAAGCTATPACTTTGGAAGGCAC	1020
Db	961	GGTGTGCAACCGGCTGATTAAGTGGTATGTTATCAAGAAGCTATPACTTTGGAAGGCAC	1020
Qy	1021	TCACCTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGT	1080
Db	1021	TCACCTGACCGAGAGGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGT	1080
Qy	1081	GAGCTTTTTCGACTTTCAGCGGATCTCTCACTGTGTTTCTGTGGTATTCGTATGTCCTT	1140
Db	1081	GAGCTTTTTCGACTTTCAGCGGATCTCTCACTGTGTTTCTGTGGTATTCGTATGTCCTT	1140
Qy	1141	TACACATGCGCAATGTTAAACGAGAGCTCAAGATAAACAACAAAGCATACCTTTGCAACT	1200
Db	1141	TACACATGCGCAATGTTAAACGAGAGCTCAAGATAAACAACAAAGCATACCTTTGCAACT	1200
Qy	1201	TTGTCAATTTCTTGGCGAGACATTTATTTCTGTGATTTTCTGTGGTATTCGTATGTCCTT	1260
Db	1201	TTGTCAATTTCTTGGCGAGACATTTATTTCTGTGATTTTCTGTGGTATTCGTATGTCCTT	1260
Qy	1261	GACAAAGTGAGATCCGTGAGTGACACACGGGAAACATCGATCGCAGTAGCTCAATCTCTA	1320
Db	1261	GACAAAGTGAGATCCGTGAGTGACACACGGGAAACATCGATCGCAGTAGCTCAATCTCTA	1320
Qy	1321	ATGGCTCTGCTCATGTTTGGAAAGAGAGCGGTTTCTGCTTTCCGTTATCGTTTCTATCTA	1380
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Qy	1381	TTAGCACAAGAGAAATCAAAAGCGAGAAATCACTTTTACATGACGAGTTGTGTTGGTGG	1440
Db	1381	TTAGCACAAGAGAAATCAAAAGCGAGAAATCACTTTTACATGACGAGTTGTGTTGGTGG	1440
Qy	1441	TCGTGCTCATGAGAGGTTCTGTATCTATGCTCTTGCATACAAACAAGTTTCAAGGGGCC	1500
Db	1441	TCGTGCTCATGAGAGGTTCTGTATCTATGCTCTTGCATACAAACAAGTTTCAAGGGGCC	1500
Qy	1501	GGGACACAGATGTACGGGAAATGCAATCATGATCAAGAGTACGATTAACCTGTCTCTT	1560
Db	1501	GGGACACAGATGTACGGGAAATGCAATCATGATCAAGAGTACGATTAACCTGTCTCTT	1560
Qy	1561	TTTAGCACAGTGGTGTGTTGTTGTTGCTGACCAAAACCACTCATAAGCTACTATTACCGAC	1620
Db	1561	TTTAGCACAGTGGTGTGTTGTTGTTGCTGACCAAAACCACTCATAAGCTACTATTACCGAC	1620
Qy	1621	CAGAACGCGCACAGAGCATGTTATCTGATGACAAACCCCAAAATCCATATATCCCT	1680
Db	1621	CAGAACGCGCACAGAGCATGTTATCTGATGACAAACCCCAAAATCCATATATCCCT	1680
Qy	1681	TTGTTGGACCAAGACTCGTTTCATTTGAGCTTTCAGGACCAACATGTCCTGGCCTGAC	1740
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Qy	1741	AGTATACGTGGCTTCTTGACACGGGCCCACTCGAAACCGGTGCAATTAATCTGGAGACAAT	1800
Db	1741	AGTATACGTGGCTTCTTGACACGGGCCCACTCGAAACCGGTGCAATTAATCTGGAGACAAT	1800
Qy	1801	GATGATCTCTTCATGCGACCCGCTTCTTGGAGAGTCTGTGGCTTTTGTACCCCTTTGTCAG	1860
Db	1801	GATGATCTCTTCATGCGACCCGCTTCTTGGAGAGTCTGTGGCTTTTGTACCCCTTTGTCAG	1860
Qy	1861	TCTCCAACTGAGAGAAAACCTCTCTGATCTTCTAGTAAAGCTTTCAGGAGTAACTGGAGAAA	1920
Db	1861	TCTCCAACTGAGAGAAAACCTCTCTGATCTTCTAGTAAAGCTTTCAGGAGTAACTGGAGAAA	1920





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Qy 961 GGTCTGCAACCGGTCTGTAAGTGCCTATGTTATCAAGAGCTATATCTTTTGGAGGCAC 1020  
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Qy 1141 TACATGCGCACATGTAACGAGAGCTCAAGATAACAAAGACATACCTTTTGCACACT 1200  
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Qy 1321 ATGGGTCTGCTCATGTTGGAAGAGCAGCGTTCGTCTTTCCGTTATGCTTTCTATCTAAC 1380  
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Qy 1501 GGGCACACAGATGACCGGGAATGCAATCATCATCAGAGTACGATAACTGTCGTCTT 1560  
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Db 1676 TTTAGCACAGTGTGTTGTATGCTGACCAAAACCACTATAAGCTACCTATPACCGCAC 1735  
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Db 1916 TTGATGACTCTTCATGCGACCGCTCTTGGAGGTGCTGTTGACCCCTTTGTTCCAG 1975  
Qy 1859 GTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAAAGGCTTGAGGGTAACGTGGAAGAA 1918  
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Qy 1919 AAGCTTTGATTTTTTTTGTAGAAAAGGTGATTCAAATTTGCTTTTGTGTAATATATC 1978  
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Qy 1979 CATTTGTAATATTTTGTGAGACAGAAATCTGCTCAACGTTTTTGAGAGCAGAGAAACA 2038  
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Qy 2039 AAACATGGCAACTTTGAAGCTTTGATTCATGTATCTAATTAATTCATATTTGTTTGT 2098  
Db 2156 AAACATGGCAACTTTGAAGCTTTGATTCATGTATCTAATTAATTCATATTTGTTTGT 2215  
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Db 2216 TGTAAACACAAACTACACATTTGTTATGTTTGAATTTGTTTTCGTAACAAAAA 2275  
Qy 2159 AAAAAAAA 2167  
Db 2276 AAAAAAAA 2284  
RESULT 3  
ABZ13434  
ID ABZ13434 standard; DNA; 1617 BP.  
XX  
AC ABZ13434;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1239.  
XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200216655-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 24-AUG-2001; 2001WO-US026685.  
XX  
PR 24-AUG-2000; 2000US-0227866P.  
PR 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX  
PA (SRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX  
DR WPI; 2002-304127/34.  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.  
XX  
PS Claim 144; SEQ ID NO 1239; 577pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office  
SQ Sequence 1617 BP; 389 A; 346 C; 359 G; 523 T; 0 U; 0 Other;  
Query Match 74.2%; Score 1617; DB 6; Length 1617;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 286 ATGTTGGATTCTTAGTGTGCAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 345  
Db 1 ATGTTGGATTCTTAGTGTGCAAACTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 60

QY 346 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGTCCTGTATTTGTTCTTTGGTCATCTTTTG 405  
Db 61 GTTGGCTTGAATCTCTTTGTTGCACTTCTTTGTCCTGTATTTGTTCTTTGGTCATCTTTTG 120  
QY 406 GAAGAGAAATAGATGAGTGAACGAATCCATCACCGCTTGTGTAATGGGCTTAGGCATCTGGT 465  
Db 121 GAAGAGAAATAGATGAGTGAACGAATCCATCACCGCTTGTGTAATGGGCTTAGGCATCTGGT 180  
QY 466 GTTACCATTGTTGTATAGTAAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 525  
Db 181 GTTACCATTGTTGTATAGTAAAGGAAAAGCTCGCATCTTCTCGTCTTTAGTGAAGAT 240  
QY 526 CTTTCTTTCATATATCTTTTGGCACCCATTAATTAATGCAGGGTTTCAAGTAAAAAAG 585  
Db 241 CTTTCTTTCATATATCTTTTGGCACCCATTAATTAATGCAGGGTTTCAAGTAAAAAAG 300  
QY 586 AAGCAGTTTTTCCGCAATTTCTGTGACTATTAATGCTTTTGGTCTGTGGGACTATTATT 645  
Db 301 AAGCAGTTTTTCCGCAATTTCTGTGACTATTAATGCTTTTGGTCTGTGGGACTATTATT 360  
QY 646 TCTTGCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAAAGTTGGACATTTGAACC 705  
Db 361 TCTTGCACAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAAAGTTGGACATTTGAACC 420  
QY 706 TTTGACTTGGTGATTAATCTTGTCTATTTGTCGCAATTTGCTGCAACAGATTCAGTATGT 765  
Db 421 TTTGACTTGGTGATTAATCTTGTCTATTTGTCGCAATTTGCTGCAACAGATTCAGTATGT 480  
QY 766 ACACTGCAGTCTCTGAATCAAGACGAGACACCTTTTGCCTTTACAGTCTTGTATTCGAGAG 825  
Db 481 ACACTGCAGTCTCTGAATCAAGACGAGACACCTTTTGCCTTTACAGTCTTGTATTCGAGAG 540  
QY 826 GGTGTTGTGAATGATCAACGTCAGTTGTGGTCTTCAACGCGAATTCAGAGCTTTTGATCTC 885  
Db 541 GGTGTTGTGAATGATCAACGTCAGTTGTGGTCTTCAACGCGAATTCAGAGCTTTTGATCTC 600  
QY 886 ACTCAGCTAAACACGAGAGCTGCTTTTCACTTTCTTGGAAACCTTCTGTATTTGTTCTC 945  
Db 601 ACTCAGCTAAACACGAGAGCTGCTTTTCACTTTCTTGGAAACCTTCTGTATTTGTTCTC 660  
QY 946 CTAAGTACCTTGTCTGGTCTGCAACCGGTCTGATAAGTCGCTATGTTATCAAGAGCTA 1005  
Db 661 CTAAGTACCTTGTCTGGTCTGCAACCGGTCTGATAAGTCGCTATGTTATCAAGAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTT 1065  
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGATGAGCGGTATCTCACTGTGTTTTTCTGTGGT 1125  
Db 781 TCTTATATGCTTGTGAGCTTTTTCGATGAGCGGTATCTCACTGTGTTTTTCTGTGGT 840  
QY 1126 ATTGTGATGTCCTTACATGCAATGTAACGAGAGGCTCAAGATTAACAACAAG 1185  
Db 841 ATTGTGATGTCCTTACATGCAATGTAACGAGAGGCTCAAGATTAACAACAAG 900  
QY 1186 CATACTTTGCAACTTTGTTCATTTCTTGGAGACATTTATTTCTTGTATGTTGGAATG 1245  
Db 901 CATACTTTGCAACTTTGTTCATTTCTTGGAGACATTTATTTCTTGTATGTTGGAATG 960  
QY 1246 GATGCTTTGGACATTCACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305  
Db 961 GATGCTTTGGACATTCACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020  
QY 1306 GTGAGCTCAATCTTAATGGTCTGCTGATGCTTGGAAAGACGCTTCTGCTTTCCGTTA 1365  
Db 1021 GTGAGCTCAATCTTAATGGTCTGCTGATGCTTGGAAAGACGCTTCTGCTTTCCGTTA 1080  
QY 1366 TCGTTTCTTATCTAATCTTAGCCAAAGAAATCAAGCGAGAAAATCACTTTTAACATGCAG 1425  
Db 1081 TCGTTTCTTATCTAATCTTAGCCAAAGAAATCAAGCGAGAAAATCACTTTTAACATGCAG 1140  
QY 1426 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGCTTCTTGCATACAAC 1485

Db 1141 GTTGTGATTTGGTGTCTGCTCTCATGAGAGGTGCTGTATCTATGCTCTTGTGATCAAC 1200  
QY 1486 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAAATGCAATCATGATCACAGGTACG 1545  
Db 1201 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAAATGCAATCATGATCACAGGTACG 1360  
QY 1546 ATAACTGTCTGTCTTTTATAGCACAGTGGTGTGTTGTTGATGCTGACCAAAACCACTCATAGC 1605  
Db 1261 ATAACTGTCTGTCTTTTATAGCACAGTGGTGTGTTGTTGATGCTGACCAAAACCACTCATAGC 1320  
QY 1606 TACCTATTACCGCACAGAACCCACACGAGCATGTATCTGATGACAAACACCCCAAAA 1665  
Db 1321 TACCTATTACCGCACAGAACCCACACGAGCATGTATCTGATGACAAACACCCCAAAA 1380  
QY 1666 TCATACATATATCCCTTTTGTGGACCAAGACTCGTTTCATTGAGCCTTTCAGGGAAACCAAT 1725  
Db 1381 TCATACATATATCCCTTTTGTGGACCAAGACTCGTTTCATTGAGCCTTTCAGGGAAACCAAT 1440  
QY 1726 GTGCTTCGCGCTGACAGTATAGTGTGCTTCTTATGACGCGCCCACTCGAACCGTGCATTAC 1785  
Db 1441 GTGCTTCGCGCTGACAGTATAGTGTGCTTCTTATGACGCGCCCACTCGAACCGTGCATTAC 1500  
QY 1786 TACTGAGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCTGTTGTTGTA 1845  
Db 1501 TACTGAGAGACAATTTGATGACTCTTTCATGCGACCGCTCTTTGGAGGTCTGTTGTTGTA 1560  
QY 1846 CCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTCTGATCTTATAGTAAAGGCTTGA 1902  
Db 1561 CCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTCTGATCTTATAGTAAAGGCTTGA 1617

## RESULT 4

ADN74230  
ID ADN74230 standard; cDNA; 1617 Bp.

AC ADN74230;

DT 15-JUL-2004 (first entry)

XX Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2125.

DE gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;  
XX growth regulator; animal feed product; thale cress;  
KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

XX Arabidopsis thaliana.

XX WO2004035798-A2.

XX 29-APR-2004.

XX 20-OCT-2003; 2003WO-BP011658.

XX 18-OCT-2002; 2002EP-00079408.

XX (CROP-) CROPDESIGN NV.

XX Inze D, De Veylder L, Vlieghe K;

XX WPI; 2004-348466/32.

DR F-PSDB; ADN74231.

XX Altering plant characteristics, useful for producing plants for enzyme or  
PT pharmaceutical production comprises modifying in a plant, expression of  
PT one or more nucleic acids and/or modifying level or activity of one or  
PT more proteins.

XX Claim 1, SEQ ID NO 2125; 134pp; English.

XX This invention relates to a novel method for altering one or more plant

CC characteristics. Specifically, it refers to identifying genes that are up

CC - or down-regulated in transgenic plants overexpressing the heterodimeric

CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
 CC alter plant characteristics accordingly. The present invention describes  
 CC generating transgenic plants for the production of growth regulators,  
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
 CC the altered plant characteristics are selected from increased yield or  
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
 CC or physiology, altered endoreplication, biochemistry, signal  
 CC transduction, storage lipid mobilization and/or altered photosynthesis,  
 CC each relative to the corresponding wild type plants. Accordingly, these  
 CC sequences can also be useful as positive or negative selectable markers  
 CC during transformation of cells or tissues. The identified genes play a  
 CC role in a variety of biological processes such as DNA replication, cell  
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
 CC transcription factors. This polynucleotide sequence is the E2Fa/Dpa  
 CC repressed 1.3 fold or more in plants overexpressing the E2Fa/Dpa  
 CC transcription factor, given in an exemplification of the invention.

XX  
 SQ Sequence 1617 BP; 389 A; 346 C; 359 G; 523 T; 0 U; 0 Other;

Query Match 74.2%; Score 1617; DB 12; Length 1617;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATTCTCTAGTGTGCGAAGCTGCTTGTGATTCGACATCTGATCAGCGTCTCTGTG 345  
 DB 1 ATGTTGGATTCTCTAGTGTGCGAAGCTGCTTGTGATTCGACATCTGATCAGCGTCTCTGTG 60  
 QY 346 GTTGGTGTGAATCTCTTGTGCACTCTTGTGCTTGTGATTCCTTGTGATCTTTTG 405  
 DB 61 GTTGGTGTGAATCTCTTGTGCACTCTTGTGCTTGTGATTCCTTGTGATCTTTTG 120  
 QY 406 GAAGAGAATAGATGGATGAACGAATCCATCAGCGCTTGTGATTCGGCTAGGCACTGGT 465  
 DB 121 GAAGAGAATAGATGGATGAACGAATCCATCAGCGCTTGTGATTCGGCTAGGCACTGGT 180  
 QY 466 GTTACCACTTGTGATAGTAAGGAAGAAAGCTCGCATCTTCTCTTGTAGTGAAGAT 525  
 DB 181 GTTACCACTTGTGATAGTAAGGAAGAAAGCTCGCATCTTCTCTTGTAGTGAAGAT 240  
 QY 526 CTTTCTTTCATATATCTTTTGGCCACCATTAATTCAGTCGAGGTTTCAAGTAAAAAAG 585  
 DB 241 CTTTCTTTCATATATCTTTTGGCCACCATTAATTCAGTCGAGGTTTCAAGTAAAAAAG 300  
 QY 586 AAGCAGTTTTCCGCAATTTCTGACTATPATGCTTTTGGTCTCTTGGGACTATATT 645  
 DB 301 AAGCAGTTTTCCGCAATTTCTGACTATPATGCTTTTGGTCTCTTGGGACTATATT 360  
 QY 646 TCTTGCACATCATATCTCTAGTGTAAACAGTCTTCTTAAAGATTTGACATTTGGAACC 705  
 DB 361 TCTTGCACATCATATCTCTAGTGTAAACAGTCTTCTTAAAGATTTGACATTTGGAACC 420  
 QY 706 TTTGACTTTGGGTGATTATCTTGCTATTGGTGCCATATTTGTCGAACAGATTTCAGTATGT 765  
 DB 421 TTTGACTTTGGGTGATTATCTTGCTATTGGTGCCATATTTGTCGAACAGATTTCAGTATGT 480  
 QY 766 AACTGCAGGTCTGAAATCAAGACGAGACACCTTTTACAGTCTTGTATTTCGAGAG 825  
 DB 481 AACTGCAGGTCTGAAATCAAGACGAGACACCTTTTACAGTCTTGTATTTCGAGAG 540  
 QY 826 GGTGTTGTGATGATCAAGCTCAGTTGTGCTTCAACGCGATTTCAGAGCTTTGATCTC 885  
 DB 541 GGTGTTGTGATGATCAAGCTCAGTTGTGCTTCAACGCGATTTCAGAGCTTTGATCTC 600  
 QY 886 ACTCAGCTAAACCAAGCTGCTTTTTCATCTTCTTGGAAAATCTTCTGTATTGTTTCTC 945  
 DB 601 ACTCAGCTAAACCAAGCTGCTTTTTCATCTTCTTGGAAAATCTTCTGTATTGTTTCTC 660  
 QY 946 CTAAGTACCTTGTGCTGCTGCAACCGGTCTGATAAGTGCCTGATGTTATCAAGAAGCTA 1005  
 DB 661 CTAAGTACCTTGTGCTGCTGCAACCGGTCTGATAAGTGCCTGATGTTATCAAGAAGCTA 720  
 QY 1006 TACTTTGGAGGCACTCAACTGACCGAGAGTTGCCCTTATGCTTATGCGGTATCTT 1065

DB 721 TACTTTGGAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGGCTATCTT 780  
 QY 1066 TCTTATATCTGCTGAGCTTTTCGACTTGGAGGTATCCTCACTGTTTCTGTTCTGCTG 1125  
 DB 781 TCTTATATCTGCTGAGCTTTTCGACTTGGAGGTATCCTCACTGTTTCTGTTCTGCTG 840  
 QY 1126 ATTGTGATGTCCTCAATTACACATGGCACAATGTAACGGAGAGCTCAAGATAAACAACAAAG 1185  
 DB 841 ATTGTGATGTCCTCAATTACACATGGCACAATGTAACGGAGAGCTCAAGATAAACAACAAAG 900  
 QY 1186 CATACCTTTGCAACTTTGTCACTTTCTGCGGAGACATTTATTTTCTGTTGTTGAATG 1245  
 DB 901 CATACCTTTGCAACTTTGTCACTTTCTGCGGAGACATTTATTTTCTGTTGTTGAATG 960  
 QY 1246 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305  
 DB 961 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020  
 QY 1306 GTGAGCTCAATCTTAATGGGCTCTGGTCACTGTTGGAAGAGCAGCGTTCCTTTTCCGTTA 1365  
 DB 1021 GTGAGCTCAATCTTAATGGGCTCTGGTCACTGTTGGAAGAGCAGCGTTCCTTTTCCGTTA 1080  
 QY 1366 TCGTTTCTATCTAACTTAGCCAAAGAAAGTAACAAAGGAGAAATCAACTTTTAACTGAG 1425  
 DB 1081 TCGTTTCTATCTAACTTAGCCAAAGAAAGTAACAAAGGAGAAATCAACTTTTAACTGAG 1140  
 QY 1426 GTTGTGATTTGGTGTCTGCTCATGAGAGGTCTGTATCTATGCTCTTCATCATCAAC 1485  
 DB 1141 GTTGTGATTTGGTGTCTGCTCATGAGAGGTCTGTATCTATGCTCTTCATCATCAAC 1200  
 QY 1486 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTAGC 1545  
 DB 1201 AAGTTTACAAGGGCCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTAGC 1260  
 QY 1546 ATAACCTGCTGCTTTTGTAGCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1605  
 DB 1261 ATAACCTGCTGCTTTTGTAGCAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1320  
 QY 1606 TACCTATTACCGCACACAGAACCGCCACACAGATGTATCTGATGACAAACCCCAAA 1665  
 DB 1321 TACCTATTACCGCACACAGAACCGCCACACAGATGTATCTGATGACAAACCCCAAA 1380  
 QY 1666 TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCACTGAGCCCTTCAGGGAAACCAAT 1725  
 DB 1381 TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCACTGAGCCCTTCAGGGAAACCAAT 1440  
 QY 1726 GTGCTCTCGGCTGACAGTATAGTGGCTTTCTTGACACCGGCCCACTCGAACCGTGCATTAC 1785  
 DB 1441 GTGCTCTCGGCTGACAGTATAGTGGCTTTCTTGACACCGGCCCACTCGAACCGTGCATTAC 1500  
 QY 1786 TACTGGAGACAATTTGATGACTCTCTCATGCGACCGCTTTTGGAGGTCTGCTGCTTTGTA 1845  
 DB 1501 TACTGGAGACAATTTGATGACTCTCTCATGCGACCGCTTTTGGAGGTCTGCTGCTTTGTA 1560  
 QY 1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTTAGTAAGGCTTTGA 1902  
 DB 1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCCCTCTGATCTTTAGTAAGGCTTTGA 1617

## RESULT 5

ADN11979

ID: ADN11979 standard; DNA; 1614 BP.

XX

AC ADN11979;

XX

DT 17-JUN-2004 (first entry)

XX

DE Wild type AtNHX1 encoding sequence.

XX

KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX

OS Arabidopsis thaliana.

XX

Key .	Location/Qualifiers	
PH	1. .1614	
FT	/*tag= a	
FT	/product= "AtNHX1"	
FT		
XX		
PN	WO2004007668-A2.	
XX		
XX		
PD	22-JAN-2004.	
XX		
XX		
PF	09-JUL-2003; 2003WO-US021549.	
XX		
PR	12-JUL-2002; 2002US-0395662P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
XX	Shi H, Blumwald E;	
XX		
DR	WPI; 2004-122911/12.	
DR	P-PSDB; ADN11980.	
XX		
PT	Enhancing salt tolerance of a plant comprises introducing into the plant	
XX	a polynucleotide encoding a Na+/H+ transporter polypeptide.	
XX		
XX	Disclosure; SEQ ID NO 1; 38pp; English.	
PS		
XX		
CC	The present invention relates to enhancing salt tolerance of a plant	
CC	comprises introducing into the plant a polynucleotide encoding a Na+/H+	
CC	transporter polypeptide. The AtNHX1 gene confers salt tolerance. The	
CC	composition and methods are useful in conferring salt tolerance on plants	
CC	and other organisms. The present sequence represents wild type AtNHX1	
XX	encoding sequence.	
XX		
XX		
XX	Sequence 1614 BP; 388 A; 346 C; 358 G; 522 T; 0 U; 0 Other;	
XX		
XX	Query Match	
XX	Best Local Similarity 74.1%; Score 1614; DB 12; Length 1614;	
XX	Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	286 ATGTGGATCTCTAGTGTGGAACCTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 345	
Db	1 ATGTGGATCTCTAGTGTGGAACCTGCTTCGTTATCGACATCTGATCAGCTTCTGTG 60	
Qy	346 GTTGGCTGAATCTCTTTGTGCACCTCTTTGTGCTGTTATGTTTCTTTGGTCACTTTTG 405	
Db	61 GTTGGCTGAATCTCTTTGTGCACCTCTTTGTGCTGTTATGTTTCTTTGGTCACTTTTG 120	
Qy	406 GAAGAGATAGATGATGAACCAATCCATCAGCGCTTGTGATTTGGCTAGGCACTGGT 465	
Db	121 GAAGAGATAGATGATGAACCAATCCATCAGCGCTTGTGATTTGGCTAGGCACTGGT 180	
Qy	466 GTTACCAATTTGTGATAGTAAAGAAAAGCTCGCATCTTCTGCTTTAGTGAAGAT 525	
Db	181 GTTACCAATTTGTGATAGTAAAGAAAAGCTCGCATCTTCTGCTTTAGTGAAGAT 240	
Qy	526 CTTTCTTCATATATCTTTGCCACCCATATATTAATCAATGCAAGGTTTCAAGTAAAAAG 585	
Db	241 CTTTCTTCATATATCTTTGCCACCCATATATTAATCAATGCAAGGTTTCAAGTAAAAAG 300	
Qy	586 AAGCAGTTTTCCGCAATTTCTGAGCATATATGCTTTTGTGCTGTTGGACATTAATT 645	
Db	301 AAGCAGTTTTCCGCAATTTCTGAGCATATATGCTTTTGTGCTGTTGGACATTAATT 360	
Qy	646 TCTTGACAAATCATATCTCTAGTGTAAACAGTTCTTTTAAAGAGTTTGGACATTTGGAACC 705	
Db	361 TCTTGACAAATCATATCTCTAGTGTAAACAGTTCTTTTAAAGAGTTTGGACATTTGGAACC 420	
Qy	706 TTTGACTTGGGTGATTATCTTGCTATTTGGTGCATATTTTGTGCAACAGATTCAGTATGT 765	
Db	421 TTTGACTTGGGTGATTATCTTGCTATTTGGTGCATATTTTGTGCAACAGATTCAGTATGT 480	
Qy	766 ACACTGAGGTTCTGAATCAAGCAGACACCTTTTGTCTTTTACGTCTTTGATTCGAGAG 825	
Db	481 ACACTGAGGTTCTGAATCAAGCAGACACCTTTTGTCTTTTACGTCTTTGATTCGAGAG 540	
Qy	826 GGTGTTGTGAATGATGCAACCGTCACTTGTGTCTTTCAACGCGATTACAGAGCTTTGATCTC 885	
Db	541 GGTGTTGTGAATGATGCAACCGTCACTTGTGTCTTTCAACGCGATTACAGAGCTTTGATCTC 600	
Qy	886 ACTCAGCTTAACCAACGAGAGCTGCTTTTCATCTTCTTGGAACCTCTTGTATTTGTTCTC 945	
Db	601 ACTCAGCTTAACCAACGAGAGCTGCTTTTCATCTTCTTGGAACCTCTTGTATTTGTTCTC 660	
Qy	946 CTAAGTACCTTGTGCTGCAACCGTCTGATAAGTGGGTATGTTATCAAGAAGCTA 1005	
Db	661 CTAAGTACCTTGTGCTGCAACCGTCTGATAAGTGGGTATGTTATCAAGAAGCTA 720	
Qy	1006 TACTTTGGAAGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCGCTATCTT 1065	
Db	721 TACTTTGGAAGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCGCTATCTT 780	
Qy	1066 TCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCCTCACTGCTGTTTTCTGTTGGT 1125	
Db	781 TCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCCTCACTGCTGTTTTCTGTTGGT 840	
Qy	1126 ATTGTGATGTCCTTATACATGCGCAATGTAAACGAGAGCTCAAGAATAACAAACAAG 1185	
Db	841 ATTGTGATGTCCTTATACATGCGCAATGTAAACGAGAGCTCAAGAATAACAAACAAG 900	
Qy	1186 CATACCTTTGCAACTTTGTCTATTTCTCGGAGACATTTATTTTCTTGTATGTTGGAATG 1245	
Db	901 CATACCTTTGCAACTTTGTCTATTTCTCGGAGACATTTATTTTCTTGTATGTTGGAATG 960	
Qy	1246 GATGCTTGGACATTTGACAGTGGAGATCCGTGATGACACACCGGAGACATCCATCGCA 1305	
Db	961 GATGCTTGGACATTTGACAGTGGAGATCCGTGATGACACACCGGAGACATCCATCGCA 1020	
Qy	1306 GTGAGCTCAATCCTAAATGGGTCTGCTCATGTTTGGAGAGCAGGTTGCTCTTTCCGTTA 1365	
Db	1021 GTGAGCTCAATCCTAAATGGGTCTGCTCATGTTTGGAGAGCAGGTTGCTCTTTCCGTTA 1080	
Qy	1366 TCGTTTCTATCTTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAATCGAG 1425	
Db	1081 TCGTTTCTATCTTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAAATCGAG 1140	
Qy	1426 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTCGTGATCTATGCTGCTTTGCTATACAC 1485	
Db	1141 GTTGTGATTTGGTGTGCTGCTCATGAGAGGTCGTGATCTATGCTGCTTTGCTATACAC 1200	
Qy	1486 AAGTTTACAAGGGCGGGGACACAGATGTACCGGGAAATGCAATCATGATCACGAGTACG 1545	
Db	1201 AAGTTTACAAGGGCGGGGACACAGATGTACCGGGAAATGCAATCATGATCACGAGTACG 1260	
Qy	1546 ATAACTGTCTGCTTTTGTAGCACAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1605	
Db	1261 ATAACTGTCTGCTTTTGTAGCACAGTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1320	
Qy	1606 TACCTATTACCGCACCAAGACGCCACACGAGAGATGTTATCTGATGACAAACCCCAAAA 1655	
Db	1321 TACCTATTACCGCACCAAGACGCCACACGAGAGATGTTATCTGATGACAAACCCCAAAA 1380	
Qy	1666 TCCATACATATCCCTTTTGTGACCCAGACCTCGTTTCAATTGAGCCCTTCAGGGAAACCAAT 1725	
Db	1381 TCCATACATATCCCTTTTGTGACCCAGACCTCGTTTCAATTGAGCCCTTCAGGGAAACCAAT 1440	
Qy	1726 GTGCTTCGCGCTTGACAGTATACGTGGCTTCTTTGACACGGCCCACTCGAAACCGTGCATTAC 1785	
Db	1441 GTGCTTCGCGCTTGACAGTATACGTGGCTTCTTTGACACGGCCCACTCGAAACCGTGCATTAC 1500	
Qy	1786 TACTGGAGACAATTTGATGACTCTCTTCAATGCGACCCGTCCTTTTGAGAGTCTGTGGCTTTGTA 1845	
Db	1501 TACTGGAGACAATTTGATGACTCTCTTCAATGCGACCCGTCCTTTTGAGAGTCTGTGGCTTTGTA 1560	
Qy	1846 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTACTAGAGGCT 1899	
Db	1561 CCCTTTGTTCCAGGTTCTCCAACTGAGAGAAACCTCTCTGATCTTAGTAGGCT 1614	

RESULT 6  
ADN11981  
ID ADN11981 standard; DNA; 1614 BP.  
XX AC  
XX ADN11981;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
XX ACHN1 mutant encoding sequence #1.  
XX  
KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.  
XX  
XX Synthetic.  
OS WO2004007668-A2.  
XX  
XX 22-JAN-2004.  
XX  
XX 09-JUL-2003; 2003WO-US021549.  
XX  
XX 12-JUL-2002; 2002US-0395662P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Shi H, Blumwald E;  
XX  
XX WPI; 2004-122911/12.  
XX  
XX P-PSDB; ADN11982.  
XX  
XX Enhancing salt tolerance of a plant comprises introducing into the plant  
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.  
XX  
XX Claim 17; SEQ ID NO 3; 38pp; English.  
XX  
XX The present invention relates to enhancing salt tolerance of a plant  
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+  
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The  
CC composition and methods are useful in conferring salt tolerance on plants  
CC and other organisms. The present sequence represents a mutant AtNHX1  
CC encoding sequence.  
XX  
XX Sequence 1614 BP; 388 A; 345 C; 359 G; 522 T; 0 U; 0 Other;  
XX  
Query Match 74.0%; Score 1612.4; DB 12; Length 1614;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1613; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 286 ATGTTGGATTCTCTAGTGTGAAACTGCGCTTCGTTATCGACATCTGATCAGCGTCTGTG 345  
DB 1 ATGTTGGATTCTCTAGTGTGAAACTGCGCTTCGTTATCGACATCTGATCAGCGTCTGTG 60  
QY 346 GTTGGCTTGAATCTCTTTGTGCACTTCTTTGTGCTTGTATGTTCTTGGTCTATCTTTG 405  
DB 61 GTTGGCTTGAATCTCTTTGTGCACTTCTTTGTGCTTGTATGTTCTTGGTCTATCTTTG 120  
QY 406 GAAGAGATAGATGAGTGAACCAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGCT 465  
DB 121 GAAGAGATAGATGAGTGAACCAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGCT 180  
QY 466 GTTACCAATTTGTGATGATGAAGAAAGTTCGCACTCTTCTCGTCTTTAGTGAAGAT 525  
DB 181 GTTACCAATTTGTGATGATGAAGAAAGTTCGCACTCTTCTCGTCTTTAGTGAAGAT 240  
QY 526 CTTTTCTTCATATCTTTTGGCCACCATTAATTAATGAGAGGTTTCAAGTAAAG 585  
DB 241 CTTTTCTTCATATCTTTTGGCCACCATTAATTAATGAGAGGTTTCAAGTAAAG 300  
QY 586 AAGCAGTTTTTCGGCAATTTCTGACTATATGCTTTTGGTCTGTTGGGACTATTAAT 645  
DB 301 AAGCAGTTTTTCGGCAATTTCTGACTATATGCTTTTGGTCTGTTGGGACTATTAAT 360  
QY 646 TCTTGACAAATCATATCTCTAGTGTAAACAGTTCCTTTAAGAAGTTGACATTTGAACC 705

DB 361 TCTTGACAAATCATATCTCTAGTGTAAACAGTTCCTTTAAGAAGTTGACATTTGAACC 420  
QY 706 TTTGACTTGGGTGATATCTTGTCTATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 765  
DB 421 TTTGACTTGGGTGATATCTTGTCTATTTGGTGCATATTTGCTGCAACAGATTCAGTATGT 480  
QY 766 ACACTGACGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTCTGATTCGAGAG 825  
DB 481 ACACTGACGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTCTGATTCGAGAG 540  
QY 826 GGTGTTGTGAATGATGCAACGTCAGTGTGTGCTTCAACGCGATTCAGAGCTTTGATCTC 885  
DB 541 GGTGTTGTGAATGATGCAACGTCAGTGTGTGCTTCAACGCGATTCAGAGCTTTGATCTC 600  
QY 886 ACTCACCTTAACCAACGAGCTGCTTTTCACTCTTTGGAACCTTCTGTTATTTGTTCTC 945  
DB 601 ACTCACCTTAACCAACGAGCTGCTTTTCACTCTTTGGAACCTTCTGTTATTTGTTCTC 660  
QY 946 CTAAGTACCTTGTGCTGCAACCGCTCTGATAAGTGCCTATCTTATCAAGAGCTA 1005  
DB 661 CTAAGTACCTTGTGCTGCAACCGCTCTGATAAGTGCCTATCTTATCAAGAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACGCGAGAGGTTGCCCTTATGATGCTTATGCGTATCTT 1065  
DB 721 TACTTTGGAAGGCACTCAACGCGAGAGGTTGCCCTTATGATGCTTATGCGTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTCACTTGAGCGGTATCTCCTGTTGTTTCTGTTGT 1125  
DB 781 TCTTATATGCTTGTGAGCTTTTCACTTGAGCGGTATCTCCTCACTGTGTTTCTGTTGT 840  
QY 1126 ATTGTGATGTCCTATTAACATGCGACCAATGTAACGAGAGCTCAAGATAACAACAAAG 1185  
DB 841 ATTGTGATGTCCTATTAACATGCGACCAATGTAACGAGAGCTCAAGATAACAACAAAG 900  
QY 1186 CATACCTTTGCAACTTTGTCTATTTCTGCGAGACATTTATTTTCTGTTATGTTGGAATG 1245  
DB 901 CATACCTTTGCAACTTTGTCTATTTCTGCGAGACATTTATTTTCTGTTATGTTGGAATG 960  
QY 1246 GATGCTTGTGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGAGACATCGATCGCA 1305  
DB 961 GATGCTTGTGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGAGACATCGATCGCA 1020  
QY 1306 GTGAGCTCAATCTTAATGGGTCTGCTCATGTTGGAAGACGAGCGTTCGTCTTTCCGTTA 1365  
DB 1021 GTGAGCTCAATCTTAATGGGTCTGCTCATGTTGGAAGACGAGCGTTCGTCTTTCCGTTA 1080  
QY 1366 TCGTTTCTATCTTAACCTTAAGCAAGAAATCAAGCGAGAAATCAACTTTTAAACATGCGAG 1425  
DB 1081 TCGTTTCTATCTTAACCTTAAGCAAGAAATCAAGCGAGAAATCAACTTTTAAACATGCGAG 1140  
QY 1426 GTTGTGATTTGTGCTGCTCTCATGAGAGTGTCTGATCTATGCTCTTGCCTCTTGCATACAC 1485  
DB 1141 GTTGTGATTTGTGCTGCTCTCATGAGAGTGTCTGATCTATGCTCTTGCCTCTTGCATACAC 1200  
QY 1486 AAGTTTACAAGGCGCGGCGCACACAGATGTACGCGGAAATGCAATCATGATCACGAGTAGC 1545  
DB 1201 AAGTTTACAAGGCGCGGCGCACACAGATGTACGCGGAAATGCAATCATGATCACGAGTAGC 1260  
QY 1546 ATAACTGTCTGCTTTTGTAGCACAGTGTGTTTGTGATGCTGACCAACCACTCATAGC 1605  
DB 1261 ATAACTGTCTGCTTTTGTAGCACAGTGTGTTTGTGATGCTGACCAACCACTCATAGC 1320  
QY 1606 TAGCTTATTTACCGCACCAAGACCGCACACAGAGATGTTTATCTGATGACCAACCCCAAAA 1665  
DB 1321 TACCTTATTTACCGCACCAAGACCGCACACAGAGATGTTTATCTGATGACCAACCCCAAAA 1380  
QY 1666 TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCTTATGAGCCCTTACGGGAACCAAT 1725  
DB 1381 TCCATACATATCCCTTTTGTGACCAAGACTCGTTTCTTATGAGCCCTTACGGGAACCAAT 1440  
QY 1726 GTGCTCGGCTGTACAGTATAGTGGCTTCTTGTACACGGCCCACTCGAACCGTGCATTTAC 1785



Db 1441 GTGCCTGGCTGACAGTATACGTGGCTTCTTGACAGGGCCACTCGAACCGTGCAATTAC 1500

Qy 1786 TACTGGAGACAATTTGATGACTCCTTCATGCGACCGCTCTTTGGAGGTCGTGCTTTGTA 1845

Db 1501 TACTGGAGACAATTTGATGACTCCTTCATGCGACCGCTCTTTGGAGGTCGTGCTTTGTA 1560

Qy 1846 CCCTTTGTTCCAGGTTCTCCACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCT 1899

Db 1561 CCCTTTGTTCCAGGTTCTCCTCACTGAGAGAAACCCCTCCTGATCTTAGTAAGGCT 1614

RESULT 7

ADN11983

ID ADN11983 standard; DNA; 1563 BP.

XX AC

XX ADN11983;

XX 17-JUN-2004 (first entry)

DT ATNHX1 mutant encoding sequence #2.

XX salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX Synthetic.

XX W02004007668-A2.

XX PN

XX PD

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021549.

XX 12-JUL-2002; 2002US-0395662P.

XX (REGC ) UNIV CALIFORNIA.

PA Shi H, Blumwald E;

XX WPI; 2004-122911/12.

DR P-PSDB; ADN11984.

XX Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide.

PT Claim 2; SEQ ID NO 5; 38pp; English.

XX The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt tolerance on plants and other organisms. The present sequence represents a mutant AtNHX1 encoding sequence.

XX Sequence 1563 BP; 376 A; 333 C; 348 G; 506 T; 0 U; 0 Other;

Query Match 71.8%; Score 1563; DB 12; Length 1563;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 286 ATGTTGGATCTCTAGTGTGAAACTGCGCTTATCGACATCTGATCAGCGTCTCTG 345

Db 1 ATGTTGGATCTCTAGTGTGAAACTGCGCTTATCGACATCTGATCAGCGTCTCTG 60

Qy 346 GTTGCCTTGAATCTCTTTGTGACATCTTTGTGCTTGTATGTTCTTGTGATCTTTTG 405

Db 61 GTTGCCTTGAATCTCTTTGTGACATCTTTGTGCTTGTATGTTCTTGTGATCTTTTG 120

Qy 406 GAAGAGATAGATGGATGAACGAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGGT 465

Db 121 GAAGAGATAGATGGATGAACGAATCCATCAGCGCTTGTGATTTGGGCTAGGCACTGGT 180

Qy 466 GTTACCAATTTGTTGATTAGTAAGGAAAGTCGCGATCTTCTGCTTTTAGTGAAGAT 525

Db 181 GTTACCAATTTGTTGATTAGTAAGGAAAGTCGCGATCTTCTGCTTTTAGTGAAGAT 240

Qy 526 CTTTCTTCATATATCTTTTGGCACCCATATATTAATCAATGACGGGTTTCAAGTAAAAAG 585

Db 241 CTTTCTTCATATATCTTTTGGCACCCATATATTAATCAATGACGGGTTTCAAGTAAAAAG 300

Qy 586 AAGCAGTTTTCGCGAAATTTCTGCTGACTATATATGCTTTTGGTGTCTCTGGGACTATTATT 645

Db 301 AAGCAGTTTTCGCGAAATTTCTGCTGACTATATATGCTTTTGGTGTCTCTGGGACTATTATT 360

Qy 646 TCTTGCAATCATATATCTTAGGTGTAAACACAGTCTCTTTAAGAAGTTGGACATTGGAACC 705

Db 361 TCTTGCAATCATATATCTTAGGTGTAAACACAGTCTCTTTAAGAAGTTGGACATTGGAACC 420

Qy 706 TTTGACTTGGGTGATTAATCTTGTCTATTTGTCCTATTTGTCGCAATTTGTCGCAATCAGTATGT 765

Db 421 TTTGACTTGGGTGATTAATCTTGTCTATTTGTCCTATTTGTCGCAATTTGTCGCAATCAGTATGT 480

Qy 766 AACTGCGAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTCTATTTCGGAGAG 825

Db 481 AACTGCGAGGTTCTGAATCAAGACGAGACACCTTTGCTTTACAGTCTTCTATTTCGGAGAG 540

Qy 826 CGTGTGTGAATGATGCAACGTCAGTTGTGGTCTTCAACGCGATTTCAGAGCTTTGATCTC 885

Db 541 CGTGTGTGAATGATGCAACGTCAGTTGTGGTCTTCAACGCGATTTCAGAGCTTTGATCTC 600

Qy 886 ACTCACCTAAACCCAGAAAGCTGCTTTTTCATCTTCTTGGAACTTCTTGTATTGTTTCTC 945

Db 601 ACTCACCTAAACCCAGAAAGCTGCTTTTTCATCTTCTTGGAACTTCTTGTATTGTTTCTC 660

Qy 946 CTAAGTACCTTCTGTTGGTCTCAACCGCTCTGATTAAGTCCGTTATTCAGAGACTA 1005

Db 661 CTAAGTACCTTCTGTTGGTCTCAACCGCTCTGATTAAGTCCGTTATTCAGAGACTA 720

Qy 1006 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGGTATCTT 1065

Db 721 TACTTTGGAAGGCACTCAACTGACGAGAGGTTGCCCTTATGATGCTTATGGGTATCTT 780

Qy 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCCTCACTGTGTTTCTGTGGT 1125

Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCCTCACTGTGTTTCTGTGGT 840

Qy 1126 ATGTGATGTCCTCATACATGCGACATGTAACGAGAGCTTCAGAGATTAACAACAAAG 1185

Db 841 ATGTGATGTCCTCATACATGCGACATGTAACGAGAGCTTCAGAGATTAACAACAAAG 900

Qy 1186 CATACCTTTGCAACTTTTGTCTTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 1245

Db 901 CATACCTTTGCAACTTTTGTCTTTCTTGGGAGACATTTATTTCTTGTATGTTGGAATG 960

Qy 1246 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305

Db 961 GATGCTTGGACATTTGACAAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020

Qy 1306 GTGAGCTCAATCTTAATGGGTCTGCTGATGTTGGAGAGCGGTCGCTTTCCGTTA 1365

Db 1021 GTGAGCTCAATCTTAATGGGTCTGCTGATGTTGGAGAGCGGTCGCTTTCCGTTA 1080

Qy 1366 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1425

Db 1081 TCGTTTCTATCTAACTTAGCCAAAGAAATCAAGCGAGAAATCAACTTTTAACATGCGAG 1140

Qy 1426 GTTGTGATTTGGTGTGCTGCTCTCATGAGAGGTCGTGATCTATGCGCTCTTTCGATACAAC 1485

Db 1141 GTTGTGATTTGGTGTGCTGCTCTCATGAGAGGTCGTGATCTATGCGCTCTTTCGATACAAC 1200

Qy 1486 AAGTTTAAAGGGCGGGGCAACAGATGACGCGGGAATGCAATCATGATCAGGATAG 1545

Db 1201 AAGTTTAAAGGGCGGGGCAACAGATGACGCGGGAATGCAATCATGATCAGGATAG 1260

Qy 1546 ATAACTGCTGCTTTTATAGCACAGTGGTGTGTTGATGCTGACCAAAACCACTCATAGC 1605

Db 1261 ATAACTGCTGCTTTTATAGCACAGTGGTGTGTTGATGCTGACCAAAACCACTCATAGC 1320



Db 1144 GCATACAAAGTTTACAGGGCGGGGCACACAGATGTACGGGGAATGCAATCATGATC 1203  
QY 1537 ACAGTAGCATAAAGTGTCTCTCTTTTATAGCACAGTGTGTGTGTATGCTGACCAACCA 1596  
Db 1204 ACCAGTACGATAAAGTGTCTCTCTTTTATAGCACAGTGTGTGTGTATGCTGACCAACCA 1263  
QY 1597 CTATAGCTACCTATTAACGGACCAAGAACGCCACACAGAGCATGTATCTGATGACAAC 1656  
Db 1264 CTATAGCTACCTATTAACGGACCAAGAACGCCACACAGAGCATGTATCTGATGACAAC 1323  
QY 1657 ACCCCAAATCCATACATATCCCTTTGTGTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGG 1716  
Db 1324 ACCCCAAATCCATACATATCCCTTTGTGTGGACCAAGACTCGTTTCATTGAGCCCTTCAGGG 1383  
QY 1717 AACCAAAATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACAGCGGCCCACTCGAACC 1776  
Db 1384 AACCAAAATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACAGCGGCCCACTCGAACC 1443  
QY 1777 GTGCATTAATCTAGTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGTCTGT 1836  
Db 1444 GTGCATTAATCTAGTGGAGACAAATTTGATGACTCTTTCATGCGACCCGCTTTTGGAGTCTGT 1503  
QY 1837 GGCTTTGTACCCCTTTGTTCAGGTTCTTCCAACTGAGAGAAACCCCTCTGATCTTAGTAAG 1896  
Db 1504 GGCTTTGTACCCCTTTGTTCAGGTTCTTCCAACTGAGAGAAACCCCTCTGATCTTAGTAAG 1563  
QY 1897 GCT 1899  
Db 1564 GCT 1566

## RESULT 9

ADN11985

ID ADN11985 standard; DNA; 1473 BP.

XX

AC ADN11985;

XX

DT 17-JUN-2004 (first entry)

XX

DE AtNHX1 mutant encoding sequence #3.

XX

KW salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX

XX Synthetic.

XX

OS WO2004/007668-A2.

XX

PN 22-JAN-2004.

XX

PD 09-JUL-2003; 2003WO-US021549.

XX

PF 12-JUL-2002; 2002US-0395662P.

XX

PR (REGC ) UNIV CALIFORNIA.

XX

PI Shi H, Blumwald E;

XX

DR WPI: 2004-122911/12.

XX

DR P-PSDB; ADN11986.

XX

PT Enhancing salt tolerance of a plant comprises introducing into the plant

XX

PS a polynucleotide encoding a Na+/H+ transporter polypeptide.

XX

PS Claim 4; SEQ ID NO 7; 38pp; English.

XX

CC The present invention relates to enhancing salt tolerance of a plant  
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+  
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The  
CC composition and methods are useful in conferring salt tolerance on plants  
CC and other organisms. The present sequence represents a mutant AtNHX1  
CC encoding sequence.

XX

SQ Sequence 1473 BP; 358 A; 306 C; 327 G; 482 T; 0 U; 0 Other;

Query Match 67.6%; Score 1473; DB 12; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 286 ATGTTGGATCTCTAGTGTGGAACCTGCTTATCGACATCTGATCAGCGTTCGTG 345  
Db 1 ATGTTGGATCTCTAGTGTGGAACCTGCTTATCGACATCTGATCAGCGTTCGTG 60  
QY 346 GTTGCCTTCAATCTCTTTGTTGTCACCTTCTTTGTCCTGTATGTTCTTGCTCATCTTTTG 405  
Db 61 GTTGCCTTCAATCTCTTTGTTGTCACCTTCTTTGTCCTGTATGTTCTTGCTCATCTTTTG 120  
QY 406 GAAGAGATAGATGGATGAACGAATCCATCAACCGCCTTGTGATGGGTAGGACATGCT 465  
Db 121 GAAGAGATAGATGGATGAACGAATCCATCAACCGCCTTGTGATGGGTAGGACATGCT 180  
QY 466 GTTACCAATTTGTTGATTAAGGAAAGAAAGCTCGCATCTCTCTCTTTAGTGAAGAT 525  
Db 181 GTTACCAATTTGTTGATTAAGGAAAGAAAGCTCGCATCTCTCTCTTTAGTGAAGAT 240  
QY 526 CTTTCTTTCATATATCTTTTGGCACCCATTAATTCATGCGAGGTTTCAAAGTAAAAAG 585  
Db 241 CTTTCTTTCATATATCTTTTGGCACCCATTAATTCATGCGAGGTTTCAAAGTAAAAAG 300  
QY 586 AAGCAGTTTTCGCAATTTCTGACTATATGCTTTTGGTCTCTTGGGACTATATT 645  
Db 301 AAGCAGTTTTCGCAATTTCTGACTATATGCTTTTGGTCTCTTGGGACTATATT 360  
QY 646 TCTTGCAATCATATCTCTAGGTGAACACAGTCTTTTAAAGAGTTGGACATTTGGAACC 705  
Db 361 TCTTGCAATCATATCTCTAGGTGAACACAGTCTTTTAAAGAGTTGGACATTTGGAACC 420  
QY 706 TTTGACTTGGGTGATTTATCTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 765  
Db 421 TTTGACTTGGGTGATTTATCTGCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGT 480  
QY 766 ACACCTGCGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGCGAGAG 825  
Db 481 ACACCTGCGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGCGAGAG 540  
QY 826 GGTGTTGTAATGATGCAACAGTGTGCTTCAACCGGATTCAGAGCTTTGATCTC 885  
Db 541 GGTGTTGTAATGATGCAACAGTGTGCTTCAACCGGATTCAGAGCTTTGATCTC 600  
QY 886 ACTCACCTAAACCAACGAGCTGCTTTTCTTCTTGGAAACTTCTGTTATTTGTTTCTC 945  
Db 601 ACTCACCTAAACCAACGAGCTGCTTTTCTTCTTGGAAACTTCTGTTATTTGTTTCTC 660  
QY 946 CTAAGTACCTTGTGTTGCTGCAACCGGCTCTGATAAGTCCGCTATCTTATCAAGAAAGCTA 1005  
Db 661 CTAAGTACCTTGTGTTGCTGCAACCGGCTCTGATAAGTCCGCTATCTTATCAAGAAAGCTA 720  
QY 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 1065  
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTT 780  
QY 1066 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTCTGTGGT 1125  
Db 781 TCTTATATGCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTGTTTCTGTGGT 840  
QY 1126 ATTGTGATGCCATTTACATGGGCAATGTAACCGAGAGCTTCAAGAAATAACAAAG 1185  
Db 841 ATTGTGATGCCATTTACATGGGCAATGTAACCGAGAGCTTCAAGAAATAACAAAG 900  
QY 1186 CATACCTTTGCAACTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGAATG 1245  
Db 901 CATACCTTTGCAACTTTGTTCATTTCTTGGGAGACATTTATTTCTTGTATGTTGAATG 960  
QY 1246 GATGCTTCGACATTTGACAAGTGGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1305  
Db 961 GATGCTTCGACATTTGACAAGTGGAGATCCGTGAGTGAGATCCGTGAGTGACACACCGGGAACATCGATCGCA 1020

QY 1306 GTGAGCTCAATCCTAATGGGCTGGTCATGGTTGGAGAGCAGGCTTCGCTTTCCGTTA 1365  
 Db 1021 GTGAGCTCAATCCTAATGGGCTGGTCATGGTTGGAGAGCAGGCTTCGCTTTCCGTTA 1080  
 QY 1366 TCGTTCTCTATCTAATCTAGCCAGAGNATCAAGCCAGAGAAATCAACTTTAAATCGAG 1425  
 Db 1081 TCGTTCTCTATCTAATCTAGCCAGAGNATCAAGCCAGAGAAATCAACTTTAAATCGAG 1140  
 QY 1426 GTTGTGATTTGGTGGTCTCTGATGAGAGGTCCTGTATCTATGGCTCTTGGCATCAAC 1485  
 Db 1141 GTTGTGATTTGGTGGTCTCTGATGAGAGGTCCTGTATCTATGGCTCTTGGCATCAAC 1200  
 QY 1486 AAGTTTCAAGGGCCGGGACACAGATGTACCGGGGAATGCAATCATGATCAGAGTACG 1545  
 Db 1201 AAGTTTCAAGGGCCGGGACACAGATGTACCGGGGAATGCAATCATGATCAGAGTACG 1260  
 QY 1546 ATAACTGCTCTCTTTTATAGCAGAGTGGTTGGTATGCTGACCAACCACTCATAGC 1605  
 Db 1261 ATAACTGCTCTCTTTTATAGCAGAGTGGTTGGTATGCTGACCAACCACTCATAGC 1320  
 QY 1606 TACCTATTACCGCACCAAGACGCCACACGAGCATGTTCTGATGACAAACCCCAAAA 1665  
 Db 1321 TACCTATTACCGCACCAAGACGCCACACGAGCATGTTCTGATGACAAACCCCAAAA 1380  
 QY 1666 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATGAGCCTTCAGGGAACCAAT 1725  
 Db 1381 TCCATACATATCCCTTTTGGACCAAGACTCGTTTCATGAGCCTTCAGGGAACCAAT 1440  
 QY 1726 GTGCTCGGCTGACATGATAGTGGCTCTTG 1758  
 Db 1441 GTGCTCGGCTGACATGATAGTGGCTCTTG 1473

RESULT 10  
 ADN11991

ID ADN11991 standard; cDNA; 1410 BP.

XX AC ADN11991;

XX DT 17-JUN-2004 (first entry)

XX DE NDL-2 encoding sequence.

XX KW salt tolerance; Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide; AtNHX1; ss.

XX OS Saccharomyces sp.

XX PN WO2004007668-A2.

XX PD 22-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021549.

XX PR 12-JUL-2002; 2002US-0395662P.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Shi H, Blumwald E;

XX PI WPI; 2004-122911/12.

XX DR P-PSDB; ADN11992.

XX PT Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup> transporter polypeptide.

XX PS Claim 4; SEQ ID NO 13; 38pp; English.

XX CC The present invention relates to enhancing salt tolerance of a plant  
 CC comprises introducing into the plant a polynucleotide encoding a Na<sup>+</sup>/H<sup>+</sup>  
 CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The  
 CC composition and methods are useful in conferring salt tolerance on plants  
 CC and other organisms. The present sequence represents NDL-2 encoding  
 CC sequence.

XX SQ Sequence 1410 BP; 348 A; 309 C; 309 G; 444 T; 0 U; 0 Other;  
 Query Match 64.6%; Score 1407; DB 12; Length 1410;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-308;  
 Matches 1407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 493 AAAAGCTCCGATCTCTCGTCTTTAGTGAAGATCTTTCTCATATATCTTTTGCCACCC 552  
 Db 4 AAAAGCTCCGATCTCTCGTCTTTAGTGAAGATCTTTCTCATATATCTTTTGCCACCC 63  
 QY 553 ATTATATTCAATGACGGGTTTCAAGTAAAGAGACAGTTCCTCCGCAATTTCTGTAAT 612  
 Db 64 ATTATATTCAATGACGGGTTTCAAGTAAAGAGACAGTTCCTCCGCAATTTCTGTAAT 123  
 QY 613 ATTATGCTTTTGGTGGTCTGTTGGGACTATATTTCTTGACAAATCATATCTCTAGGTGA 672  
 Db 124 ATTATGCTTTTGGTGGTCTGTTGGGACTATATTTCTTGACAAATCATATCTCTAGGTGA 183  
 QY 673 ACACAGTCTTTTAAAGAGTTGGACATTTGAACTTTGACTTGGGTGATTTCTTGCTATT 732  
 Db 184 ACACAGTCTTTTAAAGAGTTGGACATTTGAACTTTGACTTGGGTGATTTCTTGCTATT 243  
 QY 733 GGTGCCATATTTGCTGCAACAGATTCAATGATGACATGACAGTTCCTGAATCAAGACGAG 792  
 Db 244 GGTGCCATATTTGCTGCAACAGATTCAATGATGACATGACAGTTCCTGAATCAAGACGAG 303  
 QY 793 ACACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGTGTGTGAATGATGCAACGTCAGTT 852  
 Db 304 ACACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGTGTGTGAATGATGCAACGTCAGTT 363  
 QY 853 GTGGTCTTCAACGCGATTGAGAGCTTTGATCTCACTCACTAAACACCAAGCTGCTTTT 912  
 Db 364 GTGGTCTTCAACGCGATTGAGAGCTTTGATCTCACTCACTAAACACCAAGCTGCTTTT 423  
 QY 913 CATCTCTTTGGAAAATTCTGTGATTTGTTTCTCTAAGTACCTTCCTGGTCTGCAACC 972  
 Db 424 CATCTCTTTGGAAAATTCTGTGATTTGTTTCTCTAAGTACCTTCCTGGTCTGCAACC 483  
 QY 973 GGTCTGATAAGTGCGTATGTTATCAAGAGCTATACTTTGGAGGCACTCAACTGACCGA 1032  
 Db 484 GGTCTGATAAGTGCGTATGTTATCAAGAGCTATACTTTGGAGGCACTCAACTGACCGA 543  
 QY 1033 GAGGTTCGCTTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGTGAGCTTTTCGAC 1092  
 Db 544 GAGGTTCGCTTTATGATGCTTATGGCGTATCTTTCTTATATGCTTGTGAGCTTTTCGAC 603  
 QY 1093 TTGAGCGGTATCCTCACTGTGTTTCTGTGGTATGTGATGTCCCATTTACATGGGAC 1152  
 Db 604 TTGAGCGGTATCCTCACTGTGTTTCTGTGGTATGTGATGTCCCATTTACATGGGAC 663  
 QY 1153 AATGTAAACGAGAGCTCAAGAAATAACAAGAGCATACCTTTGCAACTTTGTCTTTCTT 1212  
 Db 664 AATGTAAACGAGAGCTCAAGAAATAACAAGAGCATACCTTTGCAACTTTGTCTTTCTT 723  
 QY 1213 GCGGAGACATTTATTTTCTGTATGTGGAAATGGATGCTTTGGACATTTGACAAGTGGAGA 1272  
 Db 724 GCGGAGACATTTATTTTCTGTATGTGGAAATGGATGCTTTGGACATTTGACAAGTGGAGA 783  
 QY 1273 TCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTAATGGTCTGGTC 1332  
 Db 784 TCCGTGAGTGACACACCGGGAACATCGATCGAGTGAGCTCAATCTAATGGTCTGGTC 843  
 QY 1333 ATGGTTGGAAGAGCAGCGTTCGTCTTTCCGTTATCGTTTCTATCTAATGACCAAGAG 1392  
 Db 844 ATGGTTGGAAGAGCAGCGTTCGTCTTTCCGTTATCGTTTCTATCTAATGACCAAGAG 903  
 QY 1393 AATCAAGCGAGAAATCAACTTTAAACATGAGGTGTGATTTGGTGGTCTGGTCTCATG 1452  
 Db 904 AATCAAGCGAGAAATCAACTTTAAACATGAGGTGTGATTTGGTGGTCTGGTCTCATG 963  
 QY 1453 AGAGTGTCTGATCTATGGCTCTTGGCATACAAAGTTTCAAGGGCCGGGACACACAT 1512

Db 964 AGAGTGCTGTATCTATGCTCTTGATACAAACAGTTTACAGGGCGGGCACACAGAT 1023  
Qy 1513 GTACGGGGAAATCAATCATGATCAGAGTACGATAACTCTGTCTTTTACACAGTG 1572  
Db 1024 GTACGGGGAAATCAATCATGATCAGAGTACGATAACTCTGTCTTTTACACAGTG 1083  
Qy 1573 GTCTTTGGTATGCTGACCAACCACTCATAGTACTTATTCGGCACAGAGCCACC 1632  
Db 1084 GTCTTTGGTATGCTGACCAACCACTCATAGTACTTATTCGGCACAGAGCCACC 1143  
Qy 1633 ACAGAGATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTGTTGGACAA 1692  
Db 1144 ACAGAGATGTTATCTGATGACAAACCCCAAAATCCATACATATCCCTTTGTTGGACAA 1203  
Qy 1693 GACTCGTTCATGAGCCTTCAGGGAACCAAAATGTGCTCGGCTGACAGTATACGTGGC 1752  
Db 1204 GACTCGTTCATGAGCCTTCAGGGAACCAAAATGTGCTCGGCTGACAGTATACGTGGC 1263  
Qy 1753 TTCTTGACACGGCCCACTCGAACCGTGCATTAATCTGAGAGACAAATTTGATGACTCCTTC 1812  
Db 1264 TTCTTGACACGGCCCACTCGAACCGTGCATTAATCTGAGAGACAAATTTGATGACTCCTTC 1323  
Qy 1813 ATCGACCCGCTCTTGGAGTCTGCTGCTTTGATCCCTTTGCTCCAGGTTCTCCAACTGAG 1872  
Db 1324 ATCGACCCGCTCTTGGAGTCTGCTGCTTTGATCCCTTTGCTCCAGGTTCTCCAACTGAG 1383  
Qy 1873 AGAAACCTCCTGATCTTTAGTAAGGCT 1899  
Db 1384 AGAAACCTCCTGATCTTAGTAAGGCT 1410

## RESULT 11

ADN11987  
ID ADN11987 standard; DNA; 1362 BP.

XX  
AC ADN11987;

XX  
DT 17-JUN-2004 (first entry)

XX  
DE AtNHX1 mutant encoding sequence #4.

XX  
DE salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ds.

XX  
OS Synthetic.

XX  
PN WO2004007668-A2.

XX  
PD 22-JAN-2004.

XX  
PF 09-JUL-2003; 2003WO-US021549.

XX  
PR 12-JUL-2002; 2002US-0395662P.

XX  
PA (REGC ) UNIV CALIFORNIA.

XX  
PI Shi H, Blumwald E;

XX  
DR WPI: 2004-122911/12.

XX  
DR P-PSDB; ADN11988.

XX  
PT Enhancing salt tolerance of a plant comprises introducing into the plant

XX  
PT a polynucleotide encoding a Na+/H+ transporter polypeptide.

XX  
PS Claim 7; SEQ ID NO 9; 38pp; English.

XX  
CC The present invention relates to enhancing salt tolerance of a plant

XX  
CC comprises introducing into the plant a polynucleotide encoding a Na+/H+

XX  
CC transporter polypeptide. The AtNHX1 gene confers salt tolerance. The

XX  
CC composition and methods are useful in conferring salt tolerance on plants

XX  
CC and other organisms. The present sequence represents a mutant AtNHX1

XX  
CC encoding sequence.

XX  
SQ Sequence 1362 BP; 329 A; 274 C; 305 G; 454 T; 0 U; 0 Other;

Query Match 62.5%; Score 1362; DB 12; Length 1362;  
Best Local Similarity 100.0%; Pred. No. 9.9e-298;  
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 286 ATGTTGGATTTCTAGTGTGCGAACTGCTTATCGACATCTGATCAAGCTTCTGTG 345  
Db 1 ATGTTGGATTTCTAGTGTGCGAACTGCTTATCGACATCTGATCAAGCTTCTGTG 60  
Qy 346 GTTGCGTTGAATCTCTTTGTCACATTTGTTGCTTGTATTGTTCTTGTGTCATCTTTG 405  
Db 61 GTTGCGTTGAATCTCTTTGTCACATTTGTTGCTTGTATTGTTCTTGTGTCATCTTTG 120  
Qy 406 GAAGAGATAGATGATGAAACGAATCCATCAACGCTTGTGTTGATTTGGGCTAGGCACTGGT 465  
Db 121 GAAGAGATAGATGATGAAACGAATCCATCAACGCTTGTGTTGATTTGGGCTAGGCACTGGT 180  
Qy 466 GTTACCATTTTGTGATTAAGGAAAGAAAGCTCGCATCTTCTGCTCTTTAGTGAAGAT 525  
Db 181 GTTACCATTTTGTGATTAAGGAAAGAAAGCTCGCATCTTCTGCTCTTTAGTGAAGAT 240  
Qy 526 CTTTCTCTCATATATCTTTTGGCCACCATTAATCAATGCAGGGTTTCAAGTAAAAAAG 585  
Db 241 CTTTCTCTCATATATCTTTTGGCCACCATTAATCAATGCAGGGTTTCAAGTAAAAAAG 300  
Qy 586 AAGCAGTTTTTCCGCAATTTGCTGACTATATGCTTTTGGTCTGTTGGGACTATTATT 645  
Db 301 AAGCAGTTTTTCCGCAATTTGCTGACTATATGCTTTTGGTCTGTTGGGACTATTATT 360  
Qy 646 TCTTGCAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAGTTGGACATTTGGAACC 705  
Db 361 TCTTGCAATCATATCTCTAGGTGTAACACAGTTCTTTAAGAGTTGGACATTTGGAACC 420  
Qy 706 TTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAAGTATGT 765  
Db 421 TTTGACTTGGGTGATTATCTTGCTATTGGTGCCATATTTGCTGCAACAGATTCAAGTATGT 480  
Qy 766 ACATCGAGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGCGAGAG 825  
Db 481 ACATCGAGTTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTGCGAGAG 540  
Qy 826 GGTGTTGTGAATGATGCAAGCTGTTGCTTCAACCGGATTTCAGAGCTTTGATCTC 885  
Db 541 GGTGTTGTGAATGATGCAAGCTGTTGCTTCAACCGGATTTCAGAGCTTTGATCTC 600  
Qy 886 ACTCACCTAAACCAAGCTGCTTTTCTATCTTTGGAACCTTCTGTTATTTGTTCTC 945  
Db 601 ACTCACCTAAACCAAGCTGCTTTTCTATCTTTGGAACCTTCTGTTATTTGTTCTC 660  
Qy 946 CTAAGTACCTTGTGCTGCTGCAACCGGTTGATTAAGTGCCTGATGTTATCAAGAGCTA 1005  
Db 661 CTAAGTACCTTGTGCTGCTGCAACCGGTTGATTAAGTGCCTGATGTTATCAAGAGCTA 720  
Qy 1006 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATCTTATGGCGTATCTT 1065  
Db 721 TACTTTGGAAGGCACTCAACTGACCGAGAGTTGCCCTTATGATCTTATGGCGTATCTT 780  
Qy 1066 TCTTATATGCTGCTGAGCTTTTTCGACTTGGAGGCTATCCTCACTGTTGTTTCTGTTGGT 1125  
Db 781 TCTTATATGCTGCTGAGCTTTTTCGACTTGGAGGCTATCCTCACTGTTGTTTCTGTTGGT 840  
Qy 1126 ATTGTGATGTCCTCATTAACATGCGCAATTAACCGAGAGCTTCAAGATAAACAACAAG 1185  
Db 841 ATTGTGATGTCCTCATTAACATGCGCAATTAACCGAGAGCTTCAAGATAAACAACAAG 900  
Qy 1186 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATG 1245  
Db 901 CATACCTTTGCAACTTTGTCATTTCTTGGGAGACATTTATTTTCTGTATGTTGGAATG 960  
Qy 1246 GATGCTTGGCAATTTGACAAAGTGGAGATCCGTGAGTGACACCGGGAACATCGATCGCA 1305  
Db 961 GATGCTTGGCAATTTGACAAAGTGGAGATCCGTGAGTGACACCGGGAACATCGATCGCA 1020

QY 1306 GTGAGCTCAATCCCTAATGGGCTCGTTCATGGTGGAAAGAGCAGCGTTTCGTTCCGTTA 1365  
Db 1021 GTGAGCTCAATCCCTAATGGGCTCGTTCATGGTGGAAAGAGCAGCGTTTCGTTCCGTTA 1080  
QY 1366 TCGTTTCTAATCTAATAGCCAGAGAAATCAAGCGAGAGAAATCAATCTTAACATGCAG 1425  
Db 1081 TCGTTTCTAATCTAATAGCCAGAGAAATCAAGCGAGAGAAATCAATCTTAACATGCAG 1140  
QY 1426 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTCGTATCTATGCGTCTTTCGATACAAC 1485  
Db 1141 GTTGTGATTTGGTGGTCTGTTCTCATGAGAGGTCGTATCTATGCGTCTTTCGATACAAC 1200  
QY 1486 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGAGTACG 1545  
Db 1201 AAGTTTCAAGGGCCGGGCAACAGATGTACGGGGGAATGCAATCATGATCAGAGTACG 1260  
QY 1546 ATAACTCTGCTCTTTTATAGCACAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1605  
Db 1261 ATAACTCTGCTCTTTTATAGCACAGTGTGTTGGTATGCTGACCAACCACTCATAGC 1320  
QY 1606 TACCTATTACCGCACAGAACGCCACCAACGAGCATGTTATCT 1647  
Db 1321 TACCTATTACCGCACAGAACGCCACCAACGAGCATGTTATCT 1362

## RESULT 12

ADN11993  
ID ADN11993 standard; cDNA; 1323 BP.

AC ADN11993;

DX 17-JUN-2004 (first entry)

DT NDL-3 encoding sequence.

DE salt tolerance; Na+/H+ transporter polypeptide; AtNHX1; ss.

KW Saccharomyces sp.

XX WO2004007668-A2.

XX 22-JAN-2004.

XX 09-JUL-2003; 2003WO-US021549.

XX 12-JUL-2002; 2002US-0395662P.

XX (REGC ) UNIV CALIFORNIA.

XX Shi H, Blumwald E;

XX WPI; 2004-122911/12.

XX P-PSDB; ADN11994.

PT Enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide.

XX Claim 7; SEQ ID NO 15; 38pp; English.

CC The present invention relates to enhancing salt tolerance of a plant comprises introducing into the plant a polynucleotide encoding a Na+/H+ transporter polypeptide. The AtNHX1 gene confers salt tolerance. The composition and methods are useful in conferring salt tolerance on plants and other organisms. The present sequence represents NDL-3 encoding sequence.

XX Sequence 1323 BP; 326 A; 290 C; 297 G; 410 T; 0 U; 0 Other;

XX Query Match 60.6%; Score 1320.4; DB 12; Length 1323;

XX Best Local Similarity 99.9%; Pred. No. 2.5e-288;

XX Matches 1321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 578 TAAAGAGAGCAGTTTTCGCAATTCGTGACTATTATGCTTTTGGTGTGGGA 637

Db 2 TGAAGAGAGCAGTTTTCGCAATTCGTGACTATTATGCTTTTGGTGTGGGA 61  
QY 638 CTAATTAATTTCTGCAATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAGTTGACAC 697  
Db 62 CTAATTAATTTCTGCAATCATATCTCTAGGTGTAAACAGTTCCTTTAAGAGTTGACAC 121  
QY 698 TTGGAACCTTTGACCTTTGGGTGATTAATCTTGTCTATTGCTGCCATATTGCTGCAACAGATT 757  
Db 122 TTGGAACCTTTGACCTTTGGGTGATTAATCTTGTCTATTGCTGCCATATTGCTGCAACAGATT 181  
QY 758 CAGTATGTACACTGACAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTAT 817  
Db 182 CAGTATGTACACTGACAGGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTAT 241  
QY 818 TCGGAGAGGTTGTGTAATGATGCAACCTCAGTGTGTGCTTCAACGGGATTCAGAGCT 877  
Db 242 TCGGAGAGGTTGTGTAATGATGCAACCTCAGTGTGTGCTTCAACGGGATTCAGAGCT 301  
QY 878 TTGATCTCACTCACTTAAACCAAGAGCTGCTTTTTCATCTTCTTGGAATCTTCTTCTATT 937  
Db 302 TTGATCTCACTCACTTAAACCAAGAGCTGCTTTTTCATCTTCTTGGAATCTTCTTCTATT 361  
QY 938 TGTTCCTCTAAGTACCTTGTGCTGCTGCAACCGGTCGTATAAGTCTGCTATGTTATCA 997  
Db 362 TGTTCCTCTAAGTACCTTGTGCTGCTGCAACCGGTCGTATAAGTCTGCTATGTTATCA 421  
QY 998 AGAAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGG 1057  
Db 422 AGAAGCTATACCTTTGGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGG 481  
QY 1058 CGTATCTTCTTATATATGCTTGTGAGCTTTTCGACTTTGACGGGTATTCCTCACTGTGTTTT 1117  
Db 482 CGTATCTTCTTATATGCTTGTGAGCTTTTCGACTTTGACGGGTATTCCTCACTGTGTTTT 541  
QY 1118 TCTGTGTTATGTTGATGCCCAATTAACAATGCAACAATGTAACGGAGAGCTCAAGAATAA 1177  
Db 542 TCTGTGTTATGTTGATGCCCAATTAACAATGCAACAATGTAACGGAGAGCTCAAGAATAA 601  
QY 1178 CAACAAGCATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTTCTGTATG 1237  
Db 602 CAACAAGCATACCTTTGCAACTTTGTCAATTTCTTGGGAGACATTTATTTTCTGTATG 661  
QY 1238 TTGGAATGGATGCTTGGACATTTGAACAAGTGAGATCCGTGAGTGACACACCGGGAACAT 1297  
Db 662 TTGGAATGGATGCTTGGACATTTGAACAAGTGAGATCCGTGAGTGACACACCGGGAACAT 721  
QY 1298 CGATCGAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTGGAAAGAGCAGGTTGCTCT 1357  
Db 722 CGATCGAGTGAGCTCAATCTTAATGGGTCTGGTCAATGGTTGGAAAGAGCAGGTTGCTCT 781  
QY 1358 TTCCGTTATCGTTTCTATCTAATTTAGCAAGAAGTAACAAGCGAGAGAAATCAACTTTA 1417  
Db 782 TTCCGTTATCGTTTCTATCTAATTTAGCAAGAAGTAACAAGCGAGAGAAATCAACTTTA 841  
QY 1418 ACATCAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTCGTCTATCTATGGCTTTG 1477  
Db 842 ACATCAGGTTGTGATTTGGTGGTCTGGTCTCATGAGAGGTCGTCTATCTATGGCTTTG 901  
QY 1478 CATACAACAGTTTACAAGGGCCGGGCAACAGATGTAGCGGGGAATGCAATCATGATCA 1537  
Db 902 CATACAACAGTTTACAAGGGCCGGGCAACAGATGTAGCGGGGAATGCAATCATGATCA 961  
QY 1538 CGAGTACCATTAATCTCTCTCTTTTACACAGTGGTGTGTTGGTATGCTGACCAACCAAC 1597  
Db 962 CGAGTACCATTAATCTCTCTCTTTTACACAGTGGTGTGTTGGTATGCTGACCAACCAAC 1021  
QY 1598 TCATAAGCTACTATTAACCGCACAGAACCGCACACGAGCATGTTATCTGATGACACA 1657  
Db 1022 TCATAAGCTACTATTAACCGCACAGAACCGCACACGAGCATGTTATCTGATGACACA 1081  
QY 1658 CCCCAAAATCATACATATCCCTTTGTTGGCAAGACTCCGTTCAATGAGCCTTCAGGGA 1717



Db 1082 CCCAAATCCATACATATCCCTTTGTTGGACCAAGACTCGTTCATTGAGCCCTTCAGGGA 1141  
Qy 1718 ACCAATGTGCTCGGCTGACAGATAGCTGGCTTCTTGACACGGCCCACTCGAACC 1777  
Db 1142 ACCAATGTGCTCGGCTGACAGATAGCTGGCTTCTTGACACGGCCCACTCGAACC 1201  
Qy 1778 TGCAATCTACTGAGACAAATTTGATGACTCCCTTCATGCGACCGCTCTTGGAGGTCGTG 1837  
Db 1202 TGCAATCTACTGAGACAAATTTGATGACTCCCTTCATGCGACCGCTCTTGGAGGTCGTG 1261  
Qy 1838 GCTTTGTACCTTTGTTCCAGGTTCTCCAACTCAGAGAAACCTCCTGATCTTAGTAAGG 1897  
Db 1262 GCTTTGTACCTTTGTTCCAGGTTCTCCAACTCAGAGAAACCTCCTGATCTTAGTAAGG 1321  
Qy 1898 CT 1899  
Db 1322 CT 1323

RESULT 13  
ID ADM68265  
XX ADM68265 standard; DNA; 1449 BP.  
AC ADM68265;  
XX DT  
XX 03-JUN-2004 (first entry)  
XX plant Na<sup>+</sup>/H<sup>+</sup> antiporter protein gene.  
DE  
XX db; gene; salt-resistance; MGX4; mangrove; drought-resistance; plant;  
KW transgenic plant; Na<sup>+</sup>/H<sup>+</sup> antiporter protein; NHX1.  
XX Unidentified.  
XX OS  
XX CN1448511-A.  
XX PN  
XX 15-OCT-2003.  
XX PD  
XX 02-APR-2002; 2002CN-00111229.  
XX PF  
XX 02-APR-2002; 2002CN-00111229.  
XX PR  
XX (ZHAN/) ZHANG H.  
XX PA  
XX Zhang H;  
XX PI  
XX WPI; 2004-091822/10.  
XX DR  
XX Salt tolerance gene MGX4 and method of breeding a salt and drought  
XX PT tolerant-plant variety.  
XX PS Disclosure; Page 10-12; 19pp; Chinese.  
XX CC  
XX The invention relates to a novel salt-resistance gene MGX4 from mangrove  
XX or other drought-resistant plant. Breeding a salt and drought resistant  
XX plant variety comprises fusing the gene with the forced constitutive  
XX expression promoter 35S to generate vector pHXZ. The gene is transfected  
XX into a recipient plant by agrobacterium mediated transfection to give a  
XX salt and drought tolerant transgenic plant. This sequence corresponds to  
XX the DNA encoding a plant MGX4 protein. The sequence is used for  
XX comparison with the Arabidopsis thaliana NHX1 gene.  
XX SQ Sequence 1449 BP; 355 A; 326 C; 304 G; 464 T; 0 U; 0 Other;

Query Match 38.9%; Score 848; DB 12; Length 1449;  
Best Local Similarity 82.0%; Pred. No. 1.6e-181;  
Matches 977; Conservative 0; Mismatches 215; Indels 0; Gaps 0;  
Qy 427 GAATCCATCACCGCTTGTGATTGGCTAGGCACTGGTGTACCATTGTTGATTAGT 486  
Db 198 GATTCCATCACCGCTTGTGATTGGCTAGGCACTGGTGTACCATTGTTGATTAGT 257  
Qy 487 AAAGGAAAAGCTCGCATCTCTCGTCTTCTTAGTGAAGATCTTTCTTCATATATCTTTTG 546

Db 258 AAAGGAAAAGCTCGCATCTCTCGTCTTCTTAGTGAAGATCTTTCTTCATATATCTTTTG 317  
Qy 547 CCAACCATATATTTCAATGCAGGGTTTCAAGTAAAAAAGAGCAGATTTTTCGCAATTTTC 606  
Db 318 CCACCCATATATTTCAATGCAGGGTTTCAAGTAAAAAAGAGCAGATTTTTCGCAATTTTC 377  
Qy 607 GTGACTATATATGCTTTTGGTGTCTGTTGGAGCTATATATTTCTTGCACAATCATATCTCTA 666  
Db 378 GTGACTATATATGCTTTTGGTGTCTGTTGGAGCTATATATTTCTTGCACAATCATATCTCTA 437  
Qy 667 GGTGTAAACACAGTTCTTTAAGAGTTGGACATTTGGAAACCTTTGACTTTGGGTGATATCTT 726  
Db 438 GGTGTAAACACAGTTCTTTAAGAGTTGGACATTTGGAAACCTTTGACTTTGGGTGATATCTT 497  
Qy 727 GCTATTGGTGCCATATTTGCTGCAACAGATTTCAAGTATGTACACTGCAGGTTCTGAAATCAA 786  
Db 498 GCTATTGGTGCCATATTTGCTGCAACAGATTTCAAGTATGTACACTGCAGGTTCTGAAATCAA 557  
Qy 787 GACGAGACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGATGCAACG 846  
Db 558 GACGAGACCTTTTGTCTTACAGTCTTGTATTCGGAGAGGGTGTGTGAATGATGCAACG 617  
Qy 847 TCAGTTGTGCTCTTCAACCGGATTCAGAGCTTTGATCTCACTCACTAAACACGAGCT 906  
Db 618 TCAGTTGTGCTCTTCAACCGGATTCAGAGCTTTGATCTCACTCACTAAACACGAGCT 677  
Qy 907 GCTTTTTCATCTTCTTGGAAACCTTCTTGTATTTGTTTCTCCTAAGTACCTTTGCTTGGTCT 966  
Db 678 GCTTTTTCATCTTCTTGGAAACCTTCTTGTATTTGTTTCTCCTAAGTACCTTTGCTTGGTCT 737  
Qy 967 GCAACCGGCTGTATAAGTGGTATGTTATCAAGAAGCTATACCTTTGGAAGGCACTCAACT 1026  
Db 738 GCAACCGGCTGTATAAGTGGTATGTTATCAAGAAGCTATACCTTTGGAAGGCACTCAACT 797  
Qy 1027 GACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTT 1086  
Db 798 GACCGAGAGTTGCCCTTATGATGCTTATGGCGTATCTTCTTATATGCTTGTGAGCTT 857  
Qy 1087 TTCGACTTCAGCGGTATCTCACTGTGTTTTTCTGTGGTATTTGTGATGTGCCATTAACA 1146  
Db 858 TTCGACTTCAGCGGTATCTCACTGTGTTTTTCTGTGGTATTTGTGATGTGCCATTAACA 917  
Qy 1147 TGGCACAATGTAAACGGAGAGCTCAAGATAACAACAAGCATACCTTTGCAACTTTGTCA 1206  
Db 918 TGGCATCAAGTGAACAGAGGATTTAAAGTTAACCAAGCATTCATTTGTAACCTTTAGGA 977  
Qy 1207 TTTCTTGGGAGACATTTATTTTCTTGTATGTTGGATGGATGCTTGGACATTTGACAAG 1266  
Db 978 TTTCAATTATCGAACTATTTCTCTGGCTCTATGTTAAACATGGATATATTGGACCTAGAGGAC 1037  
Qy 1267 TGGAGATCCGTGAGTGACACACCGGAAACATCGATCGCAGTGAGCTCAATCTTAATGGGT 1326  
Db 1038 TGGAGATTAGCTAGTACAGAGTCTTAAGACCAATTTCTGTTAACTGCATTTATTTTGACA 1097  
Qy 1327 CTGGTTCATGTTGGAAGACAGCGGTTCTGTTCCGTTATCGTTTCTATCTAATCTTAGCC 1386  
Db 1098 TTGGTTATGATTGGAAGAGTGCATTTATATCCCTTTGAAATTCGCACTCCACCTACAA 1157  
Qy 1387 AGAAGAAATCAAGCGAGAAATCAACTTAAACATGCGGTTGTGATTTGGTGGTCTGCT 1446  
Db 1158 AAAAGGGACCGCGATCCCAAGNAATCAACTTCGAAACCAACTAATCTTATGTTGCTGCTAGT 1217  
Qy 1447 CTCATCAGAGGTGCTGCTATCTATGCTCTTGGCTTTCATACAAAGTTTACAGGGCGGCGAC 1506  
Db 1218 CTCATCAGAGGACCAATTTCAAGTTGCGGTTCTTTATACCAAGTTTAAACGCACTGTGCAC 1277  
Qy 1507 ACAGATGTACGGGGAAATCAATCATGATCACGAGTACGATAACTGTGTCTTTTTTACG 1566  
Db 1278 TCTGNAATCCGACTCAATGTTCATGTTAAACCCAGCACACTTATTGTTATTCTATTCCGC 1337  
Qy 1567 ACAGTGGTGTGGTATGCTGACCAAAACCACTCATAGCTACCTATATACCGC 1618



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Db 1490 TAGTTGACCTAGTAGCTCCGATGCTTCTAAATGACCTACTCACACCGTCCATCACT 1549
Qy 1787 ACTGGAGACAAATTTGATGACTCTCTTCAATGCGACCCGCTTTTGGAGGTGCTGGCTTTTGATC 1846
Db 1550 ATTGGCGCAATTCGATGACTCTCTTCAATGCGCCGCTTTTGGTGGCGGGTTTGTGAC 1609
Qy 1847 CCTTTGTCAGGTTCTCCAACTGAGAGAAACC 1880
Db 1610 CTTTGTCCGGGTTTACCTACTGAACAAGCAC 1643

RESULT 15
AAF75765
ID AAF75765 standard; DNA; 2553 BP.
XX
AC AAF75765;
XX
DT 14-MAY-2001 (first entry)
XX
DE Gene regulating the pH of vacuoles.
XX
KW Vacuole pH regulation; flower colour; ds.
XX
OS Nierenbergia hybrida.
XX
PN WO200114560-A1.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP005722.
XX
PR 24-AUG-1999; 99JP-00236800.
XX
PA (SUNR ) SUNTORY LTD.
XX
PI Iida S, Tanaka S, Inagaki Y;
XX
DR WPI; 2001-191648/19.
XX
DR P-PSDB; AAB73253.
XX
DR
XX
PT Morning glory-originated gene encoding a protein with pH regulation
PT activity in vacuoles, useful in controlling flower color to give new
PT breeds of colorful plants for cut flowers, particularly applicable in
PT horticulture.
XX
PS Example 7; Page 45-49; 68pp; Japanese.
XX
CC The present sequence is a gene, which encodes a protein with vacuolar pH
CC regulatory activities. The gene enables flower colour to be controlled
CC via regulation of the vacuolar pH, colours can range from blue to red in
CC colour spectrum. The gene is useful in controlling flower colour to give
CC new breeds of colourful plants for cut flowers, particularly applicable
CC in horticulture
XX
SQ Sequence 2553 BP; 666 A; 487 C; 535 G; 865 T; 0 U; 0 Other;

Query Match 37.7%; Score 821.2; DB 4; Length 2553;
Best Local Similarity 70.3%; Pred. No. 2.1e-175;
Matches 1115; Conservative 0; Mismatches 468; Indels 3; Gaps 1;

Qy 289 TTGGATTCTAGTGTGAAACTCGCTTCGTTATCGACATCTGATCACGCTTCTGTGGTT 348
Db 543 TTTGGGACTCTGCTGGGAAGATGAACAACCTTAAACAACCTCTGATCATCAATCAGTGGTG 602
Qy 349 GCSTTGAATCTTTGTGACATCTTTGTGCTGTATGTTCTTGTGATCTTTGGAA 408
Db 603 TCGTAAACTTGTGTGACATTAATTTGGCGGTGATTGTGATCGGTCAATTTATTTGGAG 662
Qy 409 GAGATAGATGGATGAACGATCCATCACCGCTTGTGATTGGGCTAGGCACTGGTGT 468
Db 663 GAAAAACAGATGGATGAATGATGCCATTAACCTGCTGTTGTGATTGGTAGTTCACCTGGAGTC 722
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Qy 469 ACCATTTTGTGATTAGTAAAGGAAAAAGCTCCGATCTTCTCGTCTTTAGTGAAGATCTT 528
Db 723 ATCAATTTCTAATAAGTGGAGGAAAGAACTCAATATTTTAGTGTTCAGCGAAGATCTT 782
Qy 529 TTCTTCATATATCTTTTGGCACCACCATATATCAATGCAAGGCTTCAAGTAAAGAAAGAG 588
Db 783 TTCTTCATTTACCTTCTTCCACCGATCATTATTAATGCTGGGTTCCAGGTGAAAGAAAGAA 842
Qy 589 CAGTTTTCGCGCAATTTCCGTAATTAATGCTTTTGGTGTCTTGGGATATTAATTTCT 648
Db 843 TCATTTCTCGCAATTTTCAATGCTCTTTGGGCGAGTTGGCACCTTGATATCG 902
Qy 649 TGCACAAATCATATCTCTAGGTGTAAACACAGTCTTTAAGAGTTGGACATTTGACCTTT 708
Db 903 TTCAATTAATTAATTCAGCGGGTGTCTATTGGCAATTTCAAGAAAAATGGAATATTGGACACCTT 962
Qy 709 GACTTGGGTGATTATCTTGTCTATTGGTGCCATATTTGCTGCAACAGATTCAGTATGTACA 768
Db 963 GAAATTTGGAGATTACCTTGCATTTGGAGCAATCTTTGCTGCAACAGATTCGTATGCACC 1022
Qy 769 CTGCAAGTTCTGAATCAAGACGAGACACCTTTGCTTTTACAGTCTTGTATTCGAGAGGGT 828
Db 1023 TTACAAGTGTCTTAATCAGGAAGAAACACCGTTATTGTACAGTCTAGTGTTTGGAGAAGT 1082
Qy 829 GTTGTGAATGATGCAACAGTTCAGTGTGCTTCAACGCGGATTCAGAGCTTTGATCTCACT 888
Db 1083 GTTGTGAATGATGCCACATCTGTAGTGTCTTCAATGCTGTCCAGAACTTTTGACTTATCT 1142
Qy 889 CACCTAAACCAAGAGCTGCTTTTCAATCTTCTTGGAACTTCTTGTATTTGTTCTCCTA 948
Db 1143 CATATCAGCACAGGCAAGCTCTGCAATTAATTTGGAACCTTTCTATCTTTGTTTGCCTG 1202
Qy 949 AGTACCTTGTCTGCTGCTGCAACCGGTCTGATAGTGCGGTATGTTATCAAGAAAGCTATAC 1008
Db 1203 AGCACCTTCTAGGGGTGCTGTGGCTTACTAAGTGCCCTTTATAATTAAGAAACTCTAC 1262
Qy 1009 TTTGGAAGGCACTCAACTGACCGAGAGGTTCGCTTATGATGTTATGGGTATCTTCT 1068
Db 1263 TTTGGAAGGCACTCGACTGATCGTGGTGTCTAATGATCTATGATGCTGCGGTACCTATCA 1322
Qy 1069 TATATCTTGTGAGCTTTTTCGACTTTGAGCGGTATCTCACTGTTGTTTCTGTGGTATT 1128
Db 1323 TACATCTTGTGTAATTTATTTAAGTGGAACTCTCACTGTGTTTCTGTGGGATC 1382
Qy 1129 GTGATGTCCCAATTACACATGCGCAATGTAAACGAGAGCTCAAGAAATFAACAACAAAGCAT 1188
Db 1383 GTGATGTCTCACTATACCTGGCATAATGTCACTGAGAGCTCAAGAGTCACTACCAAGCAC 1442
Qy 1189 ACCTTTGCAACTTTGTCTTTCTTGGGAGACATTTATTTTCTTGTATGTTGGAATGGAT 1248
Db 1443 ACGTTTGTCTACATTAATCAATTTATGCTGAAATATTCATATTCCTTTATGTTGGTATGGAT 1502
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Db 1623 TTCTTGTCAACTTTGACCAAGAAAAATCCTGAGGACAAAGATTAGCTTTTAACAGCAGGTT 1682
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Qy 1489 TTTTACAAGGCGCGGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACGATA 1548
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[illegible]

Search completed: April 26, 2005, 03:59:39  
Job time : 1210 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2005, 03:32:03 ; Search time 7201 Seconds  
(without alignments)  
11512.842 Million cell updates/sec

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Perfect score: 2178  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	671.6	30.8	2080	3	AY105332	AY105332 Zea mays
2	630.6	29.0	3272	3	AY109416	AY109416 Zea mays
3	595.6	27.3	651	6	C99909	C99909 C99909 Arab
4	487.2	22.4	834	6	CA767092	CA767092 AF53-Rpf
5	478.8	22.0	1449	9	CL973674	CL973674 OsIFCC024
6	435.8	20.0	483	5	BP570332	BP570332 BP570332
7	432.8	19.9	966	7	CK260919	CK260919 EST706997
8	432	19.8	433	1	AV792419	AV792419 AV792419
9	429.4	19.7	629	1	AV825792	AV825792 AV825792
10	422.4	19.4	448	6	CD531888	CD531888 12G22 Ara
11	416.6	19.1	733	5	BU004460	BU004460 QG5E06.Y
12	416.2	19.1	827	7	CO094724	CO094724 GR_Ea17A
13	415.8	19.1	1212	2	BE420587	BE420587 HWM000.D1
14	415	19.1	827	7	CO085721	CO085721 GR_Ea03A
15	414.2	19.0	852	6	CB681657	CB681657 OSJNEF08D
16	412.4	18.9	767	7	CF479378	CF479378 RTW3_23
17	411	18.9	743	6	CA484823	CA484823 WHE4311_B
18	409.6	18.8	690	5	BQ865196	BQ865196 QGC2A03.Y
19	408	18.7	420	1	AV788758	AV788758 AV788758
20	406.2	18.7	719	4	BJ312595	BJ312595 BJ312595
21	401.4	18.4	804	7	CO100982	CO100982 GR_Eb002
22	400.8	18.4	615	5	BQ589958	BQ589958 S015138-0
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25	396.2	18.2	786	7	CF208932	CF208932 CAB20004
26	396	18.2	719	5	BU039136	BU039136 PP_LBA000
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29	380.4	17.5	772	6	CD486155	CD486155 CFUS6.4D1
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31	375.2	17.2	619	5	BU926933	BU926933 88893308
32	373	17.1	589	7	CN909560	CN909560 030123ABL
33	370	17.0	819	6	CB671396	CB671396 OSJNEG04P
34	370	17.0	833	6	CB668797	CB668797 OSJNEG16N
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40	349.8	16.1	802	5	BQ512490	BQ512490 EST619905
41	346.8	15.9	709	7	CO528231	CO528231 3530.1 18
42	345.6	15.9	664	6	CA246092	CA246092 SCEZFL508
43	345	15.8	666	6	CA216351	CA216351 SCRLFL402
44	343.8	15.8	542	7	CN890706	CN890706 010513AAX
45	343.4	15.8	706	4	BJ291707	BJ291707 BJ291707

## ALIGNMENTS

RESULT 1	AY105332	2080 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY105332				
DEFINITION	Zea mays PC0131050 mRNA sequence.				
ACCESSION	AY105332				
VERSION	AY105332.1	GI:21208410			
KEYWORDS	HTC.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	1 (bases 1 to 2080)				
AUTHORS	Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.				
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 2080)				
AUTHORS	Coe, E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.				
FEATURES	Location/Qualifiers				
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	/db_xref="taxon:4577"				
	/clone_lib="Maize Mapping Project/DuPont Consensus Library"				
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"				

ORIGIN

Query Match 30.8%; Score 671.6; DB 3; Length 2080;

Best Local Similarity 65.5%; Pred. No. 7.4e-149; Matches 1029; Conservative 0; Mismatches 534; Indels 7; Gaps 3;									
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QY	378	TGCTTGATTTGTTCTTGGTCAATCTTTTGGAGAGAAATAGATGGAAGCAATCCATCAC	437						
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Db	345	CGGCTTGTATGCGGCTCATACCGGAGGCGTCATCTCTGCTGGTTACTAATGGGACAA	404						
QY	498	CTGCAATCTCTCTCTTTAGTGAAGATCTTTTCTTCATATATCTTTTGCACCCATAT	557						
Db	405	CTCAGCAATCTCTGTTTACGAGGACCTGTTTTTTCATATATTTACTTCCGCGATAAT	464						
QY	558	ATTCAATGCAAGGTTTCAAGTAAAAAGACAGTGTTCCTCGCAATTTCTGTGACTATTAT	617						
Db	465	CTTCAATGCGGGTTTCAAGTAAAGAAAGCAATCTTCCGCAACTTTATAACGATTAT	524						
QY	618	CTTTTGTGCTGTTGGGACTATATTTCTTGGCAATCATATCTCTAGGTGTACACA	677						
Db	525	TTTGTGTTGGTCTATTGGGACTCTGATTTCTCTTTGTAATAATCTCTCTTGGTCTATGGG	584						
QY	678	GTTCTTTAAGAGTTGACATCTGCACTTTGACTTGGGTGANTTCTTCTATTTGGTGC	737						
Db	585	GTTGTTCAAGAACTTGATGTTGTCCTCGAGCTTGGGACTATCTTTCGAATTTGGTGC	644						
QY	738	CATATTTGTCGCAACAGTTCAGTATGTACACTGCAGGTTCTGAAATCAAGACGAGACAC	797						
Db	645	TATTTTCTCGGCAACAGATTCTGTTTGACCTTACAGGTGCTTAAACAGGATGAACACC	704						
QY	798	TTTGTCTTACAGTCTGTTATTCGAGAGGTTGTTGAATGATGCAAGCTCAGTTGGT	857						
Db	705	CTTACTCTATAGTCTAGTTTGGTGAAGGTTGTTAATGATGCCACATCTCTTGTGCT	764						
QY	858	CTTCAAGCGCATTCAGAGCTTTGATCTCACTCACTCACTAAACCAAGAGCTGCTTTTCATCT	917						
Db	765	CTTCAATGCAATTTGAACCTTGATATGTAATATTTGATGCTATTTGTTCTGTGTAATTT	824						
QY	918	TCTTGAAACTTCTTGTATTTGTTCTCTCAAGTACCTTCTTGGTGTGCTGCAACCGGTCT	977						
Db	825	CGTGGGAAATTTCTCTACTTGTCTTCAACAGCACATCTTGGAGTAGCTACCGGGTT	884						
QY	978	GATAAGTGGCTATGTTATCAAGAGCTATATCTTTGGAAGGCACTCACTGACCGAGAGT	1037						
Db	885	GCTTAGTGCAATCATTTATCAAGAGCTCTGTTTGGCAGACATTCACCTGATAGAGAAT	944						
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QY	1158	AACGGAGAGCTCAAGATATACAAAGACATCTTTTGGCACTTTGTGATTTCTTGGCGA	1217						
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QY	1218	GACATTTATTTCTTGTGATTTGGAATGATGCTTGGACATTTGCAAGTGGAGATCCGT	1277						
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QY	1278	GAGTGACACACCGGGAACATCGATCGC-AGTGAAGCTCAATCTTAATGGTCTGGTCATGG	1336						
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QY	1337	TTGGAAGACAGGTTTGGTCTTCTTCCGTTATCGTTTCTATCTAATCTAGCAAGAGAATC	1396						
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Db	1425	GAGTCAATGCTATCATGATCACCAGCACAGTTATTGTTGCTTATTTCAGCAAAATGGTTT	1484						
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Db	1659	TCACCGCGCACTCGCTCCGTCATCGCTTTTGGCGAAGTTTGACGATCGGTTCATGTC	1718						
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Db	1779	GTGTCCTCTGA	1788						
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LOCUS	AY109416								
DEFINITION	Zea mays CL694_1 mRNA sequence.								
ACCESSION	AY109416								
VERSION	AY109416.1	GI:21213132							
KEYWORDS	HTC								
SOURCE	Zea mays								
ORGANISM	Zea mays								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.								
REFERENCE	1 (bases 1 to 3272)								
AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.								
TITLE	Maize Mapping Project/buPont Consensus Sequences for Design of Overgo Probes								
JOURNAL	Unpublished (2002)								
REFERENCE	2 (bases 1 to 3272)								
AUTHORS	Coe,E.H.								
TITLE	Direct Submission								
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA								
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.								
FEATURES	Location/Qualifiers								
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Db	922	AGTTTCGAGGGTCACACCAAGCATGCTTTTGGCAACTTTCGTTTATCTCCGAGACTTTT	981
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Query Match	Score 630.6;	DB 3;	Length 3272;
Best Local Similarity	60.6%;		
Matches 1061; Conservative	Pred. No. 4.7e-139;		
Mismatches 0;	Mismatches 674;		
Indels 16;	Gaps 4;		

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LOCUS		651 bp	mRNA	linear
DEFINITION	C99909 Arabidopsis thaliana library EST 21-SEP-1999 thaliana cDNA clone 65, mRNA sequence.			
ACCESSION	C99909			
VERSION	C99909.1			
KEYWORDS	GI:4714029			
SOURCE	EST.			
	Arabidopsis thaliana (thale cress)			

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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 651)
Motohashi, R., Shinozaki, K. and Yamaguchi-Shinozaki, K.
Arabidopsis thaliana YAC C1C3B1 region specific cDNA, clone 2
Unpublished (1999)
Contact: Motohashi R
Laboratory of Plant Molecular Biology
Institute of Physical and Chemical Research (RIKEN)
3-1-1, Koyadai, Tsukuba 305-0074, Japan
Tel: +81-298-36-4359
Email: motohashi@rtc.riken.go.jp.

FEATURES
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QY 1285 ACACCGGAAATCGATCGCAGTGAGCTCAATCCTAATGGTCTGGTATGTTGGAAGA 1344
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QY 1465 TCTATGGCTCTTGATACAAAGTTTACAAAGGCGCGGCACACAGATGTACCGGGAAT 1524
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QY 1705 GAGCCTTCAGGGAACACACATGTGCTCGCCTGACAGTATACGTGGCTCTTGACACGG 1764
DB 480 GAGCCTTCAGGGAACACACATGTGCTCGCCTGACAGTATACGTGGCTCTTGACACGG 539

QY 1765 CCCATCGAACCGTGATTAATACT--GGAGACAAATTTGATGACTCCCTCATGCGACCCGT 1823
DB 540 SCCCTCSAACCGTGATTAATACT--GGAGACAAATTTGATGACTCCCTCATGCGACCCGT 599

QY 1824 CTTT--GGAGTCTGGGTTTGACCTTTGTT--CCAGTTCCTCAACTGAG 1872
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RESULT 4
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CA767092

LOCUS

DEFINITION

CA767092 834 bp mRNA linear EST 08-JAN-2003  
AF53-Rpf 13 P08 T7 032.ab1 IRRI Drought Stress Panicle Library  
Oryza sativa (indica cultivar-group) cDNA clone C0004976 5'. Similar  
to Sodium/hydrogen exchanger 6 (Na<sup>+</sup>/H<sup>+</sup> exchanger 6) (NHE-6),  
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CA767092.2 GI:27549114  
EST.  
Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and  
Bruskiewich, R.W.  
IRRI Drought Stress Panicle cDNA Library  
Unpublished (2002)  
On Dec 2, 2002 this sequence version replaced gi:25996347.  
Contact: Richard Bruskiewich  
Bionetrics and Bioinformatics Unit  
International Rice Research Institute  
DAPO 7777, Metro Manila, Philippines  
Tel: +63-2-845-0563  
Fax: +63-2-845-0606  
Email: r.bruskiewich@cgiar.org  
International Rice Information System (IRIS;  
<http://www.iris.irri.org>): D0204975  
Assignment of putative function to the sequence by S. Rudd of the  
Munich Information Center for Protein Sequences  
(<http://mips.gsf.de>)  
Plate: 13 row: P column: 08.

FEATURES

source

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Location/Qualifiers  
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/clone\_lib="IRRI Drought Stress Panicle Library"  
/note="Vector: pBluescript II SK+; Water stress was  
applied by not watering for 4 consecutive days. Panicles  
were collected from control (well watered) and stressed  
plants at 2 days before heading, at heading, 50% flowering  
and 4 days after 50% flowering."

ORIGIN

Query Match 22.4%; Score 487.2; DB 6; Length 834;  
Best Local Similarity 73.9%; Pred. No. 5.6e-105;  
Matches 615; Conservative 0; Mismatches 217; Indels 0; Gaps 0;  
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DB 2 GTCTGCATATGACAGTCTCAATCAGGATGAGACACCTTTTGTACAGTCTGATTC 61  
QY 820 GGAGGGGTGTGTGAATGATGTCACAGTCAGTTGGTCTTCAACCGCATTCAGAGCTTT 879  
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QY 880 GATCTCACTCACTAAACACAGAGCTGCTTTTCACTTTCTTGGAAAACCTTTGATTTTG 939  
DB 122 GATCTGTCCACATAGATGCGGCTGTCTTCTGAATTTCTTGGGAACTCTTTTATTTA 181  
QY 940 TTTCTCTTAAGTACCTTGCTTGGTCTGCTCAACCGGTCCTGATAAGTGCCTATGTTATCAAG 999  
DB 182 TTTTGTGCGAGCACCTTCTTGGAGTATTGTCTGGATTGCTCAGTGCAATACATAATCAAG 241  
QY 1000 AAGCTATATCTTGAAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGCG 1059  
DB 242 AAGCTATATCTTGAAGGCACTTACTGACCGTGGTTCCTTATGATGCTTATGCTCTATGCT 301



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Db 849 -----ACCTGCAAAATCAATGGGATAAGCTCAATTTTGTAGGATTGGT 893
QY 1332 CATGTTGGAGAGACAGGTTTCGTTTCGTTATCGTTTCTATCTAATCTAGCCAGAA 1391
Db 894 TCTGATTGGAGAGAGCTGTTTTGTTATTCGCGCTGCTGTTCTTGTGCAACCTTAAACAAGAA 953
QY 1392 GAATCAAAAGCGAGAAATCAACTTTTAAACATGACAGTTGTGATTTGGTGGTCTGCTCTCAT 1451
Db 954 GGCACCGAATGAAATAATCACTGGAGACAGCAAGTTGTAATATGTTGGCTGGCTGAT 1013
QY 1452 GAGAGGTGCTGTATCTATGCTTCTTGTGATCAACAAGTTTACAGGCGCGGACACAGA 1511
Db 1014 GAGAGGAGCTGTGTCGATGCTCTTGTCTTCAATAAAGTTTACAGATCTGCCATCTCA 1073
QY 1512 TGTAACGGGGAATCAATCATGATCAGAGTACGATTAATCTGCTCTTTTATGACAGT 1571
Db 1074 GCTCAGCGCAGTCAATAATGATCAGCAGCACCATCACTGTCGTTCTTTTATGACACTAT 1133
QY 1572 GGTGTTTGGTATGCTGACCAAAACCACTATAAGCTACTATTACCGCACCAAGAACGCCAC 1631
Db 1134 GGTATTTGGGATGATGACAAGCCATTGATCAGGCTGCTGTACCGGCTCAGGCCATCC 1193
QY 1632 CACGAGCATGTTATCTGATGACAAACCCCAAAATCATATCATATCCCTTTTGTGGACCA 1691
Db 1194 TGTCAAC-----TCTGAGGCTTTCATCACCAGTCCCTGCAATTCCTCTCTGACAAG 1247
QY 1692 AGACTGTTTATGAGGCTTCAGGACCAACAATGTGCTCGGCTGACAGATATAGTGG 1751
Db 1248 CATGCAAGGTTCTGACCTCGAGAGTACAACAACATTTGAGGCTTCAGGCTTCGGAT 1307
QY 1752 CTTCTTGACACGGCCCACTCGAACCGTGCAATTAATCTGAGAGCAAAATTTGATGACTCCTT 1811
Db 1308 GCTCCTCACCAGCGCACCACTGTCCACTACTACTGCGCAAGTTGACAGCGGCT 1367
QY 1812 CATCGGACCGCTCTTTGGAGGTGTGCTTTGTACCTTTGTTCCAGGTTCTCAACTGA 1871
Db 1368 GATCGGACCGATGTTTGGCGGCGGGTTCTGTCGCTTCTCCCTGGATCACCACCGA 1427
QY 1872 GAGAAACCT 1881
Db 1428 GCAGAGCCAT 1437

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RESULT 6
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LOCUS BP570332 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-72-D17 3',
DEFINITION mRNA sequence.
ACCESSION BP570332.1 GI:48986098
VERSION BP570332
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
TITLE Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL Science 296 (5565), 141-145 (2002)
MEDLINE 21932900
PUBMED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
reversed clone; Please visit our web site

```

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FEATURES
source
Location/Qualifiers
1..483
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL14-72-D17"
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/note="Site_1: BamHI; Site_2: SalI"
(http://pfweb.gsc.riken.go.jp/) for further details.

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Best Local Similarity 97.9%; Pred. No. 9.1e-93;
Matches 473; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 1670 TACATATCCCTTTGTTGGACCAAGACTCGTTCAATGAGCCTTCAGGGAACCAATGTG- 1728
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QY 1729 CCTCGGCTGACAGTATACGTGGCTTTTGAACACGGCCCACTCGAACCGTGAATTAATAC 1788
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QY 1789 TGGAGACAATTTGATGACTCCTTCATGACCCGCTTTTGGAGGTCTGCTTGTACCC 1848
Db 363 TGGAGACAATTTGATGACTCCTTCATGACCCGCTTTTGGAGGTCTGCTTGTACCC 304
QY 1849 TTTGTTCCAGGTTCTCCAACTGAGAAACCTCTCTGATCTTA-GTAAGGCTTGAAGGTA 1907
Db 303 TTTGTTCCAGGTTCTCCAACTGAGAAACCTCTCTGATCTTAGGTAGGCTTGAAGGTA 244
QY 1908 AGTGAAGAAAGCTTTGATTTTGTGTAAGAAAGGCTGATTCAAATTAATGCTTTTG 1967
Db 243 AGTGAAGAAAGCTTTGATTTTGTGTAAGAAAGGCTGATTCAAATTAATGCTTTTG 184
QY 1968 -TGTAATATATCCATTTGTAATATTTGTTGAGACAGAAATCTGCTCAAGTTTGA 2026
Db 183 CTGTAATATATCCATTTGTAATATTTGTTGAGACAGAAATCTGCTCAAGTTTGA 124
QY 2027 GAGCAAGAAAGCAAAACATGGCAACTTTGAAGTGTGTTGATGATGATGATGATTAATATCA 2086
Db 123 GAGCAAGAAAGCAAAACATGGCAACTTTGAAGTGTGTTGATGATGATGATGATTAATATCA 64
QY 2087 TATTTGTTTGTGTTGAACAAACTACACATTTGTTTATGTTTGAATTTGTTTGTCT 2146
Db 63 TATTTGTTTGTGTTGAACAAACTACACATTTGTTTATGTTTGAATTTGTTTGTCT 4
QY 2147 TCG 2149
Db 3 TCG 1

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LOCUS BP570332 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-72-D17 3',
DEFINITION mRNA sequence.
ACCESSION BP570332.1 GI:48986098
VERSION BP570332
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
TITLE Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL Science 296 (5565), 141-145 (2002)
MEDLINE 21932900
PUBMED 11910074
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rc.riken.go.jp
reversed clone; Please visit our web site

```

The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potat-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via http://genome.arizona.edu/orders/  
Seq primer: ATT TAG GAG ACA CTA TAG.

## FEATURES

## source

/organism="Solanum tuberosum"  
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/db\_xref="taxon:4113"  
/clone="POAB52"  
/tissue\_type="abiotic stress treated leaf and root tissue"  
/lab\_host="DH10B-Tona"  
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Abiotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d. Set 4 were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cDNA library. RNA sample."

## ORIGIN

Query Match 19.9%; Score 432.8; DB 7; Length 966;  
Best Local Similarity 66.84; Pred. No. 5.3e-92;  
Matches 647; Conservative 0; Mismatches 317; Indels 4; Gaps 2;  
QY 826 GGTGTTGTGAATGATGCAAGCTCAGTTGGTCTTCAACCGGATTCAGAGCTTTGATCTC 885  
DB 1 GGTGTTGTGAATGATGCAAGCTCAGTTGGTCTTCAACCGGATTCAGAGCTTTGATCTC 60  
QY 886 ACTCAGCTAAACCAAGCTGCTTTTCATCTTTGGAACTCTTGTATTTGTTCTC 945  
DB 61 TCTCATATCAACCAAGCTGCTTTTCATCTTTGGAACTCTTGTATTTGTTCTC 120  
QY 946 CTAAGTACCTTGGTGTGTCGACCGGCTCTAATAGTCGATGTTATCAAGAGCTA 1005  
DB 121 TCAGAGCACCCTCTTAGGGGTGTTACTGGTCTACTGAGCGCTATATAATTAAGAACTC 180  
QY 1006 TACTTTGGAGGCACTCAACTGACCGAGGTTGGCCTTATGATGCTTATGGGATCTT 1065  
DB 181 TACTTTGGAGGCACTCAACTGACCGGAGTTGGCCTTATGATGCTTATGGGATCTT 240  
QY 1066 TCTTATATGCTGCTGAGCTTTTCGACTTGGCGGTATCTCTACTGTGTTTTCTGTGGT 1125  
DB 241 TCATACATGCTTGTGATTTATCTTATTAAGTTCAATCTCACTGTGTTTTCTCGGG 300  
QY 1126 ATTGTGATGCCATTACATGGCAATGTAACGGAGAGCTCAAGAAATCAACAAG 1185  
DB 301 ATTGTGATGCTCACTACACCTGGCATAATGTGACTGAGAGCTCAAGAGTCAACCAAG 360  
QY 1186 CATACTTTCGACCTTGTCTTCTTGGGAGACATTTATTTCTGTATGTTGGATG 1245  
DB 361 CATGCTTTTGCTACATTTATCATTTATGCTGGAATATTCATTCCTTTATGTTGGATG 418

QY 1246 GATGCTTGGACATTCACAAGTGGAGATCGGTGAGTGCACACACCGGGAACATCGATCGCA 1305  
DB 419 GATGCTTGGACATTCACAAGTGGAGATTCGTAAGCGACAGCCCAATATCAGTTTCAG 478  
QY 1306 GTGAGCTCAATCTTAATGGTCTGTCATGTTGGAAAGAGCAGCGTTCGTCTTTCCGTTA 1365  
DB 479 GTTAGCTCCATCTCTGTTGGGTCTGTTTGGTGGAAAGGCGACATTTGTTTCCCTG 538  
QY 1366 TCGTTTCTATCTAATCTTAGCCAAAGAAATCAAGGAGAGAAAATCACTTTTAACATG 1425  
DB 539 TCATTTTCTCCAACTTGAAGAAGTCTCCGAGGAGAGGATTAGCTTTTAACCAAGCA 598  
QY 1426 GTTGTGATTTGGTGGTCTGCTCTCATGAGAGGTGCTGTATCTATGCTCTTGCATACA 1485  
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QY 1486 AGTTTACAAAGGCGCGGCACACAGATGTACCGGGAATGCAATCATGATCAGAGTACG 1545  
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QY 1664 AATCCATACATATCCCTTTTGGCAACAGCTCGTTTCAATGAGCTTCAGGGAACACA 1723  
DB 839 AATCCTTCAATTTGTCACCTTCTTGAAGTACACAGACTCAGAGCTGATCTGGGCA 898  
QY 1724 ATGTGCTCGGCTGACAGTATACGTGGCTTCTTGACACGGCCACTCGAACCGTGCATT 1783  
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RESULT 8  
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mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
AV792419 433 bp mRNA linear EST 29-MAR-2002  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 433)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@tc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
and XhoI was ligated to modified Lambda PUC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified pBluescript vector. Please visit our web

site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES  
source

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/clone_lib="RAF17"
/notes="Site 1: BamHI; Site 2: SalI"
cold-treated (1. 2. 5. 10. 24 hr)

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## ORIGIN

Query Match	19.8%; Score 432; DB 1; Length 433;
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Matches 432; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1718 ACCACAATGTGCTCGGCCCTGACAGTATACGTGCGTCTTTGACACGCCCCACATCGAACCG 1777
Db	433 ACCACAATGTGCTCGGCCCTGACAGTATACGTGCGTCTTTGACACGCCCCACATCGAACCG 374
QY	1778 TGCATTACTACTGGAGACAAATTTGATGACATCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 1837
Db	373 TGCATTACTACTGGAGACAAATTTGATGACTCTCTTCATGCGACCCGCTTTTGGAGGTCGTG 314
QY	1838 GCTTTGTACCCCTTTGTTTCAGAGTTCCTCCAACCTGAGAGAACCCCTCTCTGATCTTTAGTAAGG 1897
Db	313 GCTTTGTACCCCTTTGTTTCAGAGTTCCTCCAACCTGAGAGAACCCCTCTCTGATCTTTAGTAAGG 254
QY	1898 CTTGAGGGTAAACGTGGAAGAAAGCTTTGATTTTTTTTGGTAGAAAGGGTGATTCAAAT 1957
Db	253 CTTGAGGGTAAACGTGGAAGAAAGCTTTGATTTTTTTTGGTAGAAAGGGTGATTCAAAT 194
QY	1958 TATGCTTTTGTGTAAATTTATCCATTTGTGTAATATGTTTCTGTGAGGACAGAAATCTGTCCTTA 2017
Db	193 TATGCTTTTGTGTAAATTTATCCATTTGTGTAATATGTTTGTGAGGACAGAAATCTGTCCTTA 134
QY	2018 ACGTTTGTGAGCAGAAAGCAAAACATGCGCACTTTTGAAGTGTTTGAATGATGATGTAA 2077
Db	133 ACGTTTGTGAGCAGAAAGCAAAACATGCGCACTTTTGAAGTGTTTGAATGATGATGTAA 74
QY	2078 TTATATTTCATATTGTTTGTGTTGTAACACAACTACACATTTGTTTATCTGTTTGAATTTG 2137
Db	73 TTATATTTCATATTGTTTGTGTTGTAACACAACTACACATTTGTTTATGTTTGAATTTG 14
QY	2138 GTTTTGTGCTTCG 2149
Db	13 GTTTTGTGCTTCG 2

RESULT 9  
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 LOCUS  
 DEFINITION  
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 AV825792 RAFL7 Arabidopsis thaliana CDNA clone RAFL07-14-P04 5',  
 mRNA sequence.  
 AV825792.1 GI:19867852  
 EST.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
 1 (bases 1 to 629)  
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Ono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
 Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
 and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 Unpublished (2002)  
 Contact: Motoaki Seki  
 COMMENT

Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda PLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

**FEATURES**

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1. 629
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/db_xref="taxon:3702"
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/dev_stage="rosette plants"
/lab_host="DH10B"
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/notes="Site 1: BamHI; Site 2: SalI;
cold-treated (1, 2, 5, 10, 24 hr

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## ORIGIN

Query Match	19.7%;	Score 429.4;	DB 1;	Length 629;
Best Local Similarity	98.0%;	Pred. No. 3.2e-91;		
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187	CCTCTCTGTTTCGGTTCCTCGTAGACGAAGAAGAAATCTCAGGTTTTAGCTTTTCGA	246		
61	AGCTTCCAAAATTTTGAATTTTGATCTCTCTGGGCTCTTTTGTAATCAGACTGGAAGATAT	120		
247	AGCTTCCAAAATTTTGAATTTTGATCTCTCTGGGCTCTTTTGTAATCAGACTGGAAGATAT	306		
121	TTAGANTATCCCAAGAATGTTTCAAGGAATGTTTTCAGTGGCAGCACGGAAGAGATAAAG	180		
307	TTAGANTATCCCAAGAATGTTTCAAGGAATGTTTTCAGTGGCAGCACGGAAGAGATAAAG	366		
181	AGACTTTTTTTTTCCAGATTTTGCTGATCCAAAATCTGAATAGTGTTCATGTTCTGGAT	240		
367	AGACTTTTTTTTTCCAGATTTTGCTGATCCAAAATCTGAATAGTGTTCATGTTCTGGAT	426		
241	CAAACTCTCGAAGAGGAATGTTGTTGGATCTAGAAGAAGATAACAATGTTGGATTCCTTA	300		
427	CAAACTCTCGAAGAGGAATGTTGTTGGATCTAGAAGAAGATAACAATGTTGGATTCCTTA	486		
301	GTGTCGAAATCGCCTTCGTTATTCGACATCTGATCACGCTTCGTGGTTCGGTGAATCTTC	360		
487	GTGTCGAAATCGCCTTCGTTATTCGACATCTGATCACGCTTCGTGGTTCGGTGAATCTTC	546		
361	TTTGTGTGCACATCTTTGTGCTGTGATTCGTTCTTGTGTCATCTTTTGGAGAGAAATAGATGG	420		
547	TTTGTGTGCACATCTTTGTGCTGTGATTCGTTCTTGTGTCATCTTTTGGAGAGAAATAGATGG	606		
421	ATGAACGAATCCATCACCGCCT	442		
607	GTGAACGAATCCATCACCGCCT	628		

## RESULT 10

CD531888

LOCUS

### DEFINITION

3', mRNA sequence.

**ACCESSION**

VERSION CD531888.1 GI:40451900

## KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM





QY 563 ATGAGGTTTCAAGTAAAGAGAGAGTTTCCGCAATTTCTGCTACTATTATGCTTT 622  
 DB 287 ATGCTGGTTTCAAGTAAAGAGAGAGCAATTTTCCGCAATTTCTGCTACTATTATGCTTT 346  
 QY 623 TTGTGCTGTTGGGCACTATTATTCTTCTGCAATCATATCTCTAGGTTGAACACAGTTCT 682  
 DB 347 TTGTGCTGTTGGGCACTGATATCTTTTCCACATCATATCAATTTGGTGTCTATAAATTT 406  
 QY 683 TTAAGAGTTGGACATTTGGACCTTTGACTTGGGTGATATCTGCTATTGGTGCCATAT 742  
 DB 407 TCCAAGAGTGGATTTGGTACCCCTTGAGCTTGGAGACTTTCTTGCATTTGGTGAATAT 466  
 QY 743 TTGCTGCAACAGATTTCACTGACCTGCAAGTTCTGAATCAAGACGACACCTTTTC 802  
 DB 467 TTTCAAGCCAGATTCGTTGCACTTTGCAAGTTGATCAGATCAGACACCTTTAT 526  
 QY 803 TTTACAGTCTTTGATTCGAGAGGTTGTTGAATGATCAACGTCAGTTGCTCTTCA 862  
 DB 527 TATATAGTTTGGTGTGGTGAAGTTGTTGAATGATGCCATCAGTTGTCATCTTCA 586  
 QY 863 ACGGATTCAGAGCTTTGATCTCACTCACTCAACACGAGCTGCTTTTCACTTTCTTG 922  
 DB 587 ATGAGTTCAAACTTTGATCTCTCAATCACTCACTGCTGTTGCAATTTCAACTGATG 646  
 QY 923 GAAACTTCTTTGATTTCTTCTTAAGTACCTTGTGCTGCTGCAACCGGCTCTGATTA 982  
 DB 647 GAAATTTCTTTATTTATTCATCACAAGCACACTTTCTAGAGCTGGGCTACTTAA 706  
 QY 983 GTGGTATGTTATCAAGAGCTATFAC 1009  
 DB 707 GTGCTTATATATAAGAGCTATATT 733

# RESULT 12 LOCUS

DEFINITION GR\_Eal7A01.r GR\_Ea Gossypium raimondii cDNA clone GR\_Eal7A01.3', mRNA sequence.

ACCESSION CO094724.1 GI:48793410

VERSION EST.

KEYWORDS Gossypium raimondii

SOURCE Gossypium raimondii

ORGANISM Gossypium raimondii

REFERENCE 1 (bases 1 to 827)  
 Kim, H., Yu, X., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and Wing, R. A.  
 Global assembly of Cotton ESTs

AUTHORS Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu

Plate: 17 row: A column: 01.

Location/Qualifiers

1. .827

/organism="Gossypium raimondii"

/mol\_type="mRNA"

/db\_xref="taxon:29730"

/tissue\_type="whole seedlings"

/dev\_stage="first true leaves"

/lab\_host="DH10B"

/clone\_lib="GR\_Ea"

/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by invitrogen with RNA supplied by

source

1. .827

/organism="Gossypium raimondii"

/mol\_type="mRNA"

/db\_xref="taxon:29730"

/tissue\_type="whole seedlings"

/dev\_stage="first true leaves"

/lab\_host="DH10B"

/clone\_lib="GR\_Ea"

/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by invitrogen with RNA supplied by

source

## ORIGIN

Query Match 19.1%; Score 416.2; DB 7; Length 827;  
 Best local Similarity 70.5%; Pred. No. 4.7e-88;  
 Matches 556; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 973 GGTCTGATTAAGTCGCTATGTTATCAAGAAGCTATATCTTTGGAAGGCACTCAACTGACCGA 1032  
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 QY 1033 GAGTTGCCCTTATGATGCTTATGGCGTATCTTTCTTATATGCTTCTGAGCTTTTCGAC 1092  
 DB 97 GAATTTGCTTATGATGCTTATGGCAATCTTTTGTATATCATGCTGAACATGTTCTAT 156  
 QY 1093 TTGAGCGGTATCTCACTGCTGTTTTCTGTGTATTTGATGTCCTCATCATCATGCGAC 1152  
 DB 157 TTGAGTGGCATTTCTACAGTATTTCTTTTGTGGATTTGTGATTCATTTATACCTGGCAC 216  
 QY 1153 AATGTAACGGAGGCTCAAGATTAACAACAAAGCATACCTTTTGCAACTTTGTCTATTTCT 1212  
 DB 217 AATGTTACAGAGATTTCAAGAGTTACTACAAAGCATGCTTTGCTACCTTTGTCTATTT 276  
 QY 1213 GCGGAGACATTTATTTTCTTGTATGTTGAAATGGATGCTTGGACATTCGACAAAGTGACA 1272  
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 DB 817 CTCTTACA 825

## RESULT 13

BE420587

LOCUS

DEFINITION

BE420587

ACCESSION

VERSION

KEYWORDS

BE420587 1212 bp mRNA linear EST 24-JUL-2000  
 HWM000.D12 ITC HWM Barley Leaf Library Hordeum vulgare subsp.  
 vulgaris cDNA clone HWM000.D12, mRNA sequence.  
 BE420587  
 BE420587.1 GI:9418430  
 EST.

SOURCE  
ORGANISM  
Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE  
AUTHORS  
1 (bases 1 to 1212)  
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Perchionni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.  
TITLE  
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Herrmann RG  
Botanisches Institut der LMU  
Menzinger Str. 67, D-80638 Munchen GERMANY  
Fax: 49 30 171683  
Email: hermann@botanik.biologie.uni-muenchen.de  
International Triticeae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.  
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Best Local Similarity 69.1%; Pred. No. 6.2e-88;  
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QY 647 CTTCACAATCATATCTAGGTGTAAACACAGTTCTTAAAGAGTTGGACATTTGGAACCT 706  
DB 121 CCTTCAGTATATATCACTTGTGTCATGGGCTAGTATCAAGCTGAACATAGGCGCCC 180  
QY 707 TTGACTTGGGTGATATCTTGTCTATTGTTGGTGCATATTTGCTGCAACAGATTTCAGTATGTA 766  
DB 181 TTGAGCTTGGAGACTACCTCGCACTTGGGCAATATCTCGGCAACGGACTCTCTTCGCA 240  
QY 767 CACTGCAGTTTGAATCAAGACGACACCTTTGCTTTACAGTCTTGATTCGGAGAGG 826  
DB 241 CCTTCAGGTGTTAAOCCAAGATGAGACACCTTTCTTTGACAGTTTGGTGGTGGTGAAG 300  
QY 827 GTGTTCTGAATGATCAACCTCAGTTGTGCTCTTCAACGGATTTCAGAGCTTTGATCTCA 886  
DB 301 GTGTTGTTAAAGATGCGACATCAGTTGTGTTGTTCAATGCAATCCAGAACTTTGATCTTG 360  
QY 887 CTCACCTAAACACCAAGAGCTGCTTTTCATCTCTTCGGAACCTTTCTGATTTGTTTCTCC 946  
DB 361 GAAATTTTCAGTAGCCTCAAAATCTTACAAATTCATTCGGAATTTCTCTATCTATTGGCG 420  
QY 947 TAAGTACCTTGTGTTGCTGCAACCGGCTCTGATTAAGTGGTATGTTATCAAGAAGCTAT 1006  
DB 421 CCAGTACCTTTCTTGGAGTATCTAGTGGACTTCTCAGTGTATGTCATCAAGAAACTGT 480  
QY 1007 ACTTTGGAGGCACTCAACTGACCGAGAGGTTGCCCTTATGATGCTTATGGGCTATCTTT 1066  
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QY 1247 ATGCTTTGACATTTGACAGTGGAGATCGGTGAGTG-----ACACACCGGGAACATCGAT 1301  
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QY 1302 CGCAGTGAGCTCAATCCTAATCGGTCTGCTCATGTTGGAAGAGCAGCGTTCCTCTTCC 1361  
DB 781 TGCCTTGAGCTCCATTTATTTTGGCGTGTGCTGTTGCAAGAGCTGCAATTTGTTTCC 840  
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DB 841 TCTATCTATCTCTCC--AATTGACCAAAAAAATCCAGGCGAGAGATCTCTCTTAGGCA 898  
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RESULT 14  
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DEFINITION  
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ACCESSION  
CO085721.1 GI:48776355  
KEYWORDS  
EST.  
SOURCE  
Gossypium raimondii  
ORGANISM  
Gossypium raimondii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids II; Malvales; Malvaceae; Malvaceae; Gossypium. 1 (bases 1 to 827)  
REFERENCE  
AUTHORS  
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C., Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A.  
TITLE  
Global assembly of Cotton ESTs  
JOURNAL  
COMMENT  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
Plate: 03 row: A column: 21.  
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/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Clones plated/picked by AGI. More glycerol clones held in -80."  
ORIGIN  
Query Match 19.1%; Score 415; DB 7; Length 827;

Best Local Similarity		71.3%;	Pred. No. 9e-88;	Matches 547; Conservative 0; Mismatches 220; Indels 0; Gaps 0;	
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QY	940	TTTCTCCTAAGTACCTTTGCTGTCGCAACCGCTCTGATAAGTGCATGTTATCAAG	999		
Db	61	TTCACTCTCAGTACTTTTGTAGGAGTTGTGACTGGAGCTGCTCAGTCTTCATTATATA	120		
QY	1000	AAGCTATACCTTTGGAAGGCACTCACTGACGAGAGGTTGCCCTTATGATGCTTATGGCG	1059		
Db	121	AAGCTGATTTTGGGAAGGCACTCACTGATCGGAGGTTGCTCTTATGATCCTCATGGCT	180		
QY	1060	TATCTTTCTTATATGCTTGTGAGCTTTTCGACTTTGAGCGGTATCCTCACTGTGTTTTC	1119		
Db	181	TACTCTCATACATGCTCGTGAATTTCTATTTAAGCGAATCTTACAGTATCTTTT	240		
QY	1120	TGTGGTATGTGATGTCCTCCATTTACATATGCGCAATGTAAACGGAGAGCTCAAGAATAACA	1179		
Db	241	TGTGGGATTTGTATGCTCTCACTATACATGCGCAATGTAAACGGAGAGCTCAAGAATAACA	300		
QY	1180	ACAAAGCATACCTTTGCACTTTGTCATTTCTTCCGAGAGCATTTATTTCTGTATGTT	1239		
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QY	1240	GGAATGATGCTTTGGACATTTGCAAGTGGAGATCCGTGAGTGACACACCGGGAACATCG	1299		
Db	361	GGTATGATGCTTTGGACATCGAGAGTGGAGATTTATCACTGATAGCCCCGGAAATCA	420		
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QY	1360	CCGTATGCTTTCTATCTACTTTAGCAAGCAAGCAATCAAGCGAGAAATCACTTTTAAAC	1419		
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QY	1480	TACAAAGTTTACAGGGCCGGGACACAGATGTACGGGGAAATGCAATCATGATCAGC	1539		
Db	601	TATAATCAGTTTACTAGTTTAGGGCATCTCAAGTGCAGGGAAATGCGATGATGATAAC	660		
QY	1540	AGTACGATACCTCTGCTCTTTTACGACAGTGGTGTGTTGTTGATGCTGACCAACCACTC	1599		
Db	661	AGCACAATCAGGTTGTTCTTTTCAGCAGAGTGGTTTCGGATTGATGACTAAACCATTA	720		
QY	1600	ATAAGCTACCTATTACCGCACAGAAACGCCACCAGCAGCATGTTATC	1646		
Db	721	GTTAGGATCTTGCTTCTCTCTCCAAACATCTCTCGAGATGCTTTC	767		

RESULT 15  
CB681657  
LOCUS  
DEFINITION  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 852)  
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,  
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.  
Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea		Unpublished (2003)	
Contact: Rod Wing		Arizona Genomics Institute	
University of Arizona		Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ	
85721-0088, USA		Tel: 520 626 3967	
Fax: 520 621 9288		Email: http://genome.arizona.edu	
PCR Primers		FORWARD: gta aaa cga cgg cca gtg	
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QY	745	GCTGCAACAGATTTCACTATGTACACTGCGAGTTCTGAAATCAAGACGAGACACCTTTGCTT	804
Db	62	TCAGCAACAGATTTCTGTTTGACCTTACAGGTCTTACCAAGACGAAACACCCCTACTC	121
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Db	182	GCAATGAAGACATTTGATTTGCTAAATTTGATAGCTTGTCTTACTAGCGTTTCATAGA	241
QY	925	AACTTCTTGTATTTGTTTCTCTTAAGTACTTGTGCTTGGTGTGCTGCAACCGGTCTGATAAGT	984
Db	242	AAATTTCTCTACCTATTTCTTCCAGTACCTTCTTGGAGTAGTTGCTGGGTGCTTAGT	301
QY	985	GGTATGTTTCAAGAACCTATACTTTGGAAGGCACTCAACTGACGAGAGTTGCCCTT	1044
Db	302	GCCTATATTATTAAGAACTATGTTTGGCAGACACTCAACTGACAGAGAACTTGTCTATC	361
QY	1045	ATGATGCTTATGGGCTATCTTTCTTATATGCTGCTGAGCTTTTCGACTTTCGAGCGGTATC	1104
Db	362	ATGATACTCATGGCGTACTTTTCATATATGCTGCTGATGCTGCTAGTAGTCTGAGTGGCAT	421
QY	1105	CTCACTGTGTTTCTGTTGTTATTTGTGATGTCCTCCATTTACATATGACGACAAATGTAA	1164
Db	422	CTCACTGTGTTTCTCTCTGGAATAGTAAATGTACATTTACCTTTGSCATAATGTGACAGAA	481
QY	1165	AGCTCAAGAAATTAACAAAGCATACCTTTGCAACTTTGTCTTCTTTGCGGAGACATTT	1224
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QY	1225	ATTTTCTTGTATTTGGAATGGATGCTTGGACATTTGACATTTGAGATGCGTGTAGTGAC	1284
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